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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 20:26:59 ; Search time 189 Seconds

(without alignments)
169.292 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 1 cggaccctagagcaag 18

Scoring table: IDENTITY NUC

Gapop 10-0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	100.0	4094 2	US-08-571-758-5 Sequence 5, Appl1
2	18	100.0	4094 2	US-08-909-984A-5 Sequence 5, Appl1
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5	15.4	85.6	29889 3	US-09-949-016-13682 Sequence 13682, A
6	15.4	85.6	97195 3	US-09-949-016-12212 Sequence 12212, A
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9	15	83.3	50 3	US-09-513-999C-28900 Sequence 28900, A
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166	13.8	76.7	39498	3	US-09-949-016-12410	Sequence 12410, A	C 239	13.4	74.4	601	3	US-09-949-016-88950	Sequence 88950, A
167	13.8	76.7	39498	3	US-09-949-016-16505	Sequence 16505, A	C 240	13.4	74.4	601	3	US-09-949-016-124252	Sequence 124252, A
168	13.8	76.7	44120	3	US-09-949-016-14151	Sequence 14151, A	C 241	13.4	74.4	601	3	US-09-949-016-151498	Sequence 151498, A
169	13.8	76.7	44120	3	US-09-949-016-14152	Sequence 14152, A	C 242	13.4	74.4	601	3	US-09-949-016-186054	Sequence 186054, A
170	13.8	76.7	44120	3	US-09-949-016-14153	Sequence 14153, A	C 243	13.4	74.4	658	3	US-09-533-559-6647	Sequence 6647, Ap

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4094 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-909-984-5

Query Match 100.0%; Score 18; DB 2; Length 4094;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCCCTAGAGGCAAG 18
Db 296 CGACCCCTAGAGGCAAG 313

RESULT 3
US-08-909-983-5
Sequence 5, Application US/08909983
Patent No. 5747288
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
TITLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,983
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,758
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4094 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-909-983-5

Query Match 100.0%; Score 18; DB 2; Length 4094;

Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCCCTAGAGGCAAG 18
Db 296 CGACCCCTAGAGGCAAG 313

RESULT 4
US-09-621-976-17349/C
Sequence 17349, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent .pm
SEQ ID NO 17349
LENGTH: 543
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17349

Query Match 85.6%; Score 15.4; DB 3; Length 543;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GACCCCTAGAGGCAAG 18
Db 488 GACCCCTAGAGGCAAG 472

RESULT 5
US-09-949-016-13682
Sequence 13682, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13682
LENGTH: 29889
TYPE: DNA
ORGANISM: Human
US-09-949-016-13682

Query Match 85.6%; Score 15.4; DB 3; Length 29889;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GACCCCTAGAGGCAAG 18
Db 29541 GACCCCTAGAGGCAAG 29557

RESULT 6
US-09-949-016-12212/C

Sequence 12212, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12212
LENGTH: 97195
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) .. (97195)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12212

Query Match 85.6%; Score 15.4; DB 3; Length 97195;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
DB 77970 GGACCTTAGAGGCAAG 77954

RESULT 7
US-09-949-016-16971/c
Sequence 16971, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16971
LENGTH: 97196
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) .. (97196)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16971

Query Match 85.6%; Score 15.4; DB 3; Length 97196;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
DB 77970 GGACCTTAGAGGCAAG 77954

RESULT 8
US-10-131-827-7589
Sequence 7589, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
FILE REFERENCE: 50661200120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7589
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-7589

Query Match 83.3%; Score 15; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCA 16
DB 18 GGACCTTAGAGGCA 32

RESULT 9
US-09-513-999C-28900
Sequence 28900, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59 US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 28900
LENGTH: 163
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-28900

Query Match 83.3%; Score 15; DB 3; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCA 16
DB 148 GGACCTTAGAGGCA 162

RESULT 10
US-09-157-910-6
Sequence 6, Application US/09157910A
Patent No. 6197744
GENERAL INFORMATION:

APPLICANT: Berleth, Erica
APPLICANT: Burke, M. Jane
APPLICANT: Nadadur, Srikanth
APPLICANT: Gurtoo, Hira
APPLICANT: Henn, Alicia
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitory Protein TIP-B1 and Method
FILE OF INVENTION: of Using Same
FILE REFERENCE: RPP:151-US
CURRENT APPLICATION NUMBER: US/09/157,910A
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 97 / MS-DOS Ver. 7.10
SEQ ID NO 6
LENGTH: 783
TYPE: DNA
ORGANISM: HOMO SAPIENS
FEATURE:
OTHER INFORMATION: This sequence encodes the TIP-B1 peptides of SEQ. ID. #3,
US-09-157-910-6

Query Match 83.3%; Score 15; DB 3; Length 783;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCA 16
Db 730 GGACCTAGAGGCA 744

RESULT 11
US-09-484-9708-159
Sequence 159, Application US/094849708
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmutch, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,9708
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 159
LENGTH: 868
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 234571.8
NAME/KEY: unsure
LOCATION: 23, 27
OTHER INFORMATION: a, c, g, or other
US-09-484-9708-159

Query Match 83.3%; Score 15; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCA 16
Db 820 GGACCTAGAGGCA 834

RESULT 12
US-09-023-655-508
Sequence 508, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cooke, Benjamin G.
APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 508:
SEQUENCE CHARACTERISTICS:
LENGTH: 2399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MPMGNOT02
CLONE: 201392
US-09-023-655-508

Query Match 83.3%; Score 15; DB 3; Length 2399;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGACCTAGAGGCA 16
Db 2294 GGACCTAGAGGCA 2308

RESULT 13
US-09-949-016-23074/C
Sequence 23074, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23074
LENGTH: 601
TYPE: DNA

ORGANISM: Human
US-09-949-016-23074

Query Match 82.2%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGGCGCAAG 18
Db 190 CAGACCTTAGGCGCAAG 173

RESULT 14

US-09-949-016-169781/c
Sequence 169781, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 169781
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-169781

Query Match 82.2%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGGCGCAAG 18
Db 190 CAGACCTTAGGCGCAAG 173

RESULT 15

US-08-571-758-7
Sequence 7, Application US/08571758
Patent No. 570675
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Wasserman, David A.
TITLE OF INVENTION: A No. 570675el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-571-758-7

Query Match 82.2%; Score 14.8; DB 2; Length 2846;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGGCGCAAG 18
Db 214 CAGACCTTAGGCGCAAG 231

RESULT 16

US-08-909-984A-7
Sequence 7, Application US/08909984A
Patent No. 5747275
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Wasserman, David A.
TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,984A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-909-984A-7

Query Match 82.2%; Score 14.8; DB 2; Length 2846;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 214 CGGACCTTAGAGGCAAG 231

RESULT 17
US-08-909-983-7
Sequence 7, Application US/08909983
Patent No. 5747288
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Mastraman, David A.
TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,983
FILING DATE: 12-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,758
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-909-983-7
Query Match 82.2%; Score 14.8; DB 2; Length 2846;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 214 CGGACCTTAGAGGCAAG 231
RESULT 18
US-09-560-385A-23
Sequence 23, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 3585
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (60)..(3581)

CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 3469
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3465)
US-09-560-385A-23

Query Match 82.2%; Score 14.8; DB 3; Length 3469;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 1816 CGGACCTTAGAGGCAAG 1833

RESULT 19
US-09-560-385A-19
Sequence 19, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 3511
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(3507)
NAME/KEY: misc_feature
LOCATION: (13)..(36)
US-09-560-385A-19

Query Match 82.2%; Score 14.8; DB 3; Length 3511;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CGGACCTTAGAGGCAAG 18
Db 1858 CGGACCTTAGAGGCAAG 1875

RESULT 20
US-09-560-385A-21
Sequence 21, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 3585
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (60)..(3581)

NAME/KEY: sig_peptide
LOCATION: (60)..(116)
US-09-560-385A-21

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3585;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18
Db 1932 CGGATCCTAGATGCAAG 1949

RESULT 21
US-09-560-385A-17
Sequence 17, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boulard, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 3621
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (60)..(3617)
NAME/KEY: sig_peptide
LOCATION: (60)..(110)
NAME/KEY: misc feature
LOCATION: (123)..(146)
US-09-560-385A-17

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Qy 1 CGGACCTAGAGGCAAG 18
Db 1968 CGGATCCTAGATGCAAG 1985

RESULT 22
US-09-560-385A-15
Sequence 15, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boulard, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 3759
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3459)
US-09-560-385A-15

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18

Db 1810 CGGATCCTAGATGCAAG 1827

RESULT 23
US-09-560-385A-13
Sequence 13, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boulard, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 3930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (121)..(3630)
NAME/KEY: sig_peptide
LOCATION: (121)..(171)
US-09-560-385A-13

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3930;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGGCAAG 18
Db 1981 CGGATCCTAGATGCAAG 1998

RESULT 24
US-08-144-121-1
Sequence 1, Application US/08144121
Patent No. 5610031
GENERAL INFORMATION:
APPLICANT: Burgeson, Robert E.
APPLICANT: Magman, David W.
TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MCH-0780.0) MGP-021
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 122..3617
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 173..3617
US-08-144-121-1

Query Match 82.2%; Score 14.8; DB 2; Length 3931;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGCAAG 18
DB 1976 CGGATCCTAGATGCAAG 1993

RESULT 25
US-08-735-893-1
Sequence 1, Application US/08735893
Patent No. 5914317
GENERAL INFORMATION:
APPLICANT: Burgess, Robert E.
APPLICANT: Magman, David W.
TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,893
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/144,121
FILING DATE: 27-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: (MCH-0780.1) MGP-021DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 122..3617
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 173..3617
US-08-735-893-1

Query Match 82.2%; Score 14.8; DB 2; Length 3931;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGCAAG 18
DB 1976 CGGATCCTAGATGCAAG 1993

RESULT 26
US-10-841-139-1
Sequence 1, Application US/10841139
Patent No. 6916631
GENERAL INFORMATION:
APPLICANT: Burgess, Robert E.
APPLICANT: Magman, David W.
TITLE OF INVENTION: BLK CHAIN OF LAMININ AND METHODS OF USE
FILE REFERENCE: 10287/021003
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US/10/443,349
PRIOR FILING DATE: 2003-05-22
PRIOR APPLICATION NUMBER: US/09/161,872
PRIOR FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: US 08/735,893
PRIOR FILING DATE: 1996-10-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3931
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: (122)..(3616)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (173)..(3616)
US-10-841-139-1

Query Match 82.2%; Score 14.8; DB 3; Length 3931;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGCAAG 18
DB 1976 CGGATCCTAGATGCAAG 1993

RESULT 27
US-09-876-176-1
Sequence 1, Application US/09876176
Patent No. 6586244
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Den-Otter, Douglas R.
APPLICANT: Winter, Jill A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: NEOPLASTIC DISEASES USING INHIBITORS OF LAMININBETA3
FILE REFERENCE: PP-01702.002/200130.523
CURRENT APPLICATION NUMBER: US/09/876,176
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3971
TYPE: DNA
ORGANISM: Homo sapiens
US-09-876-176-1

Query Match 82.2%; Score 14.8; DB 3; Length 3971;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGCAAG 18

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US-09-919-172-15
; Sequence 15, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faxis, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 4108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 3615080CB1
US-09-919-172-15

Query Match      82.2%; Score 14.8; DB 3; Length 4108;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGGACCTAGAGCAAG 18
Db      2065 CGGATCCTAGATGCAAG 2082
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RESULT 29
US-07-841-646-3
; Sequence 3, Application US/07841646
; Patent No. 5266683
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OKAYMAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; * CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,646
; FILING DATE: 19920221
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162

; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDWARD R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17410 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3192..3730
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; OTHER INFORMATION: /note= "START CODON BEGINS AT POSITION 3313"
; FEATURE:
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; OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
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; NAME/KEY: exon
; LOCATION: 10696..10891
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10960..10961
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OTHER INFORMATION: THIS SEQUENCE."
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NAME/KEY: exon
LOCATION: 11059..11211
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NAME/KEY: misc feature
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NAME/KEY: exon
LOCATION: 11420..11617
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US-07-841-646-3

Query Match 82.2% Score 14.8; DB 2; Length 17410;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGACCTAGAGCAAG 18
DB 14427 CAGACCTAGAGCAAG 14444

RESULT 30
US-08-147-023-3
Sequence 3, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
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NAME/KEY: misc feature
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LOCATION: 11059..11211
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NAME/KEY: misc_feature
LOCATION: 11351..11352
OTHER INFORMATION: //label= GAP-3
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LOCATION: 11420..11617
OTHER INFORMATION: //label= EXON-4
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NAME/KEY: misc_feature
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THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: //label= EXON-5
FEATURE:
NAME/KEY: exon
LOCATION: 15044..15160
OTHER INFORMATION: //label= EXON-6
FEATURE:
NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: //label= EXON-7
US-08-147-023-3

Query Match 82.2%; Score 14.8; DB 2; Length 17410;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGCAAG 18
Db 14427 CAGACCTAGAGCAAG 14444
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Job time : 205 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 19:30:59 ; Search time 673 Seconds
(without alignments)
178.253 Million cell updates/sec

Title: US-10-727-358-5
Perfect score: 18
Sequence: 1 cggaccctcagagcgaag 18

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	15.4	85.6	376	6	ABL69201 Prostata
15	15.4	85.6	388	10	ADP80786 Leukaemia
16	15.4	85.6	514	4	AAK88398 Human dig
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18	15.4	85.6	514	9	ADP82225 Human nov
19	15.4	85.6	986	10	ADP82177 Leukaemia

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C 26	15	83.3	50	12	ADP10220	Adp10220 50-mer o1
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C 32	15	83.3	345	6	ABL38407	AbL38407 Human col
C 33	15	83.3	412	9	ACH49943	Ach49943 Human leu
C 34	15	83.3	444	6	ABK36157	Abk36157 CDNA sequ
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C 36	15	83.3	478	9	ACH29337	Ach29337 Human adu
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C 40	15	83.3	554	10	ADB45528	AdB45528 Human car
C 41	15	83.3	554	13	ADJ06946	Adj06946 Human car
C 42	15	83.3	627	10	ADB47513	AdB47513 Human CDN
C 43	15	83.3	645	9	AAK57225	Aak57225 Human CGD
C 44	15	83.3	764	12	ADP10552	Adp10552 Reference
C 45	15	83.3	765	3	AAA59670	Aa559670 DNA encod
C 46	15	83.3	779	6	ABK36158	Abk36158 CDNA sequ
C 47	15	83.3	782	5	AAH68582	Aah68582 Human pro
C 48	15	83.3	783	3	AAA14823	Aa14823 DNA encod
C 49	15	83.3	784	6	ABA98935	AbA98935 Human TGF
C 50	15	83.3	803	14	AEA20476	Aea20476 Novel hum
C 51	15	83.3	825	14	AEA19346	Aea19346 Novel hum
C 52	15	83.3	868	6	ABE70502	AbE70502 Human bon
C 53	15	83.3	2278	11	ADM01377	Adm01377 Human CDN
C 54	15	83.3	2399	11	ADI31182	Adi31182 Human CDN
C 55	15	83.3	2399	13	ADS83249	AdS83249 Human lym
C 56	15	83.3	5760	4	ABL17686	AbL17686 Drosophil
C 57	15	83.3	44749	11	ACN44034	Acn44034 Human gen
C 58	15	83.3	110000	13	ABD32627	Abd32627 Continuation (3 of
C 59	15	83.3	122937	13	ABD33516	Abd33516 Human can
C 60	14.8	82.2	399	3	AAA82091	Aa82091 N. mening
C 61	14.8	82.2	1115	13	ADK64023	AdK64023 Plant ful
C 62	14.8	82.2	1149	9	ADA48879	Ada48879 Banana ge
C 63	14.8	82.2	1149	11	ACL31234	AcL31234 Rice abio
C 64	14.8	82.2	2005	13	ADR62571	AdR62571 Cotton CD
C 65	14.8	82.2	2204	6	ABK35181	Abk35181 Human CDN
C 66	14.8	82.2	2204	3	AAA53270	Aa53270 Human pho
C 67	14.8	82.2	2605	8	ACG77209	AcG77209 Thiermus s
C 68	14.8	82.2	2661	9	ADA15655	Ada15655 Human kin
C 69	14.8	82.2	2703	9	ADA15657	Ada15657 Human kin
C 70	14.8	82.2	2846	2	AAT72156	Aat72156 Human Ksr
C 71	14.8	82.2	2870	4	ABLI5818	AbL15818 Drosophil
C 72	14.8	82.2	3006	4	ABL16372	AbL16372 Drosophil
C 73	14.8	82.2	3011	12	ADO36007	Ado36007 Novel mou
C 74	14.8	82.2	3342	13	ADP08122	Adp08122 Full leng
C 75	14.8	82.2	3357	12	ADG64764	AdG64764 Novel hum
C 76	14.8	82.2	3469	3	AAAC83728	Aaac83728 Human lam
C 77	14.8	82.2	3511	3	AAAC83726	Aaac83726 Human lam
C 78	14.8	82.2	3516	2	AAV29044	Aav29044 Open read
C 79	14.8	82.2	3519	14	ADV67470	Adv67470 Nucleotid
C 80	14.8	82.2	3585	3	AAAC83727	Aaac83727 Human lam
C 81	14.8	82.2	3621	3	AAAC83725	Aaac83725 Human lam
C 82	14.8	82.2	3759	3	AAAC83724	Aaac83724 Human lam
C 83	14.8	82.2	3810	8	ACCT20088	Acct20088 Human NOV
C 84	14.8	82.2	3930	3	AAO89871	Aao89871 Laminin B
C 85	14.8	82.2	3930	3	AAAC83723	Aaac83723 Human lam
C 86	14.8	82.2	3971	6	AAAD28066	Aaad28066 LamininB
C 87	14.8	82.2	3971	8	ABX76133	Abx76133 Lung can
C 88	14.8	82.2	3971	8	ACCT20087	Acct20087 Human NOV
C 89	14.8	82.2	3971	10	ADCO1884	Adco1884 Human DNA
C 90	14.8	82.2	3971	11	ADN39001	Adn39001 Cancer/an
C 91	14.8	82.2	3971	13	ACN37576	Acn37576 Tumour-ab
C 92	14.8	82.2	3971	13	ACN37576	Acn37576 Tumour-ab

93	14.8	82.2	4108	6	ABSG62737	AbBg62737	Prostate	C 166	14.4	80.0	103747	6	ABG88139	AbG88139	Human oest
94	14.8	82.2	4108	8	ABX77550	AbX77550	Different	C 167	14.4	80.0	110000	12	ADN46845_17	ADN46845_17	Continuation (18 o
95	14.8	82.2	4108	8	ABX63559	AbX63559	Human CDN	C 168	14.4	80.0	110000	12	ADN47591_03	ADN47591_03	Continuation (4 of
96	14.8	82.2	4108	14	ADV85764	ADV85764	Human CDN	C 169	14.4	80.0	110000	12	ADN46123_17	ADN46123_17	Continuation (18 o
97	14.8	82.2	4667	2	AAV29043	AAV29043	Human pro	C 170	14.4	80.0	110000	12	ADN47209_03	ADN47209_03	Continuation (4 of
98	14.8	82.2	4816	10	ADBS4538	ADBS4538	Rat gene	C 171	14.4	80.0	110000	12	ADN46464_17	ADN46464_17	Continuation (18 o
99	14.8	82.2	4816	10	ADBS4542	ADBS4542	Rat gene	C 172	14.4	80.0	110000	12	ADN47960_03	ADN47960_03	Continuation (4 of
100	14.8	82.2	5913	12	ADJ96596	ADJ96596	Human tyr	C 173	14.4	80.0	110000	14	ABE42401_21	ABE42401_21	Continuation (22 o
101	14.8	82.2	17350	2	AAO72708	AAO72708	hOP1 huma	C 174	14.4	80.0	115218	8	ACA64845	ACA64845	Human HNR
102	14.8	82.2	17410	2	AAO53142	AAO53142	Sequence	C 175	14.4	80.0	116704	11	ACN44818	ACN44818	Human gen
103	14.8	82.2	17410	2	AAAT18381	AAAT18381	hOP-1 gen	C 176	14.4	80.0	127767	13	ABD33584	ABD33584	Murine ca
104	14.8	82.2	17410	2	AAV15205	AAV15205	Human oest	C 177	14.4	80.0	127767	13	ADBS67023	ADBS67023	Murine ca
105	14.8	82.2	17410	2	AAV02730	AAV02730	Human oest	C 178	14.4	80.0	127767	14	ADZ13356	ADZ13356	Murine ca
106	14.8	82.2	17410	2	AAZ27575	AAZ27575	Human oest	C 179	14.4	80.0	134499	3	AAF22286	AAF22286	BAC conta
107	14.8	82.2	17410	10	ADJ62678	ADJ62678	Human oest	C 180	14.4	80.0	142976	13	ABD32612	ABD32612	Human can
108	14.8	82.2	17410	12	ADBS2749	ADBS2749	Human oest	C 181	14.4	80.0	150201	14	ADZ13203	ADZ13203	Human can
109	14.8	82.2	17410	12	ADM80487	ADM80487	Human oest	C 182	14.4	80.0	329019	13	ABD32707	ABD32707	Human can
110	14.8	82.2	17410	13	ADDO3609	ADDO3609	Genomic D	C 183	14.4	77.8	247	247	AAO14378	AAO14378	M. capsul
111	14.8	82.2	17415	2	AAV11639	AAV11639	Human oest	C 184	14.4	77.8	315	6	ABQ90769	ABQ90769	Rat seque
112	14.8	82.2	17415	2	AAV80733	AAV80733	Human oest	C 185	14.4	77.8	585	6	ABK62977	ABK62977	AbK62977
113	14.8	82.2	17415	2	AAA59897	AAA59897	Human DNA	C 186	14.4	77.8	585	10	ADB57048	ADB57048	AbD57048
114	14.8	82.2	97700	10	ADL13678	ADL13678	Osteoarthritis	C 187	14.4	77.8	585	12	ADP72219	ADP72219	Renal tox
115	14.8	82.2	101786	3	AAE22293	AAE22293	BAC conta	C 188	14.4	77.8	616	13	AAFO9798	AAFO9798	Fusarium
116	14.8	82.2	110000	12	ADO79173_3	ADO79173_3	Continuation (4 of	C 189	14.4	77.8	616	13	ADU53839	ADU53839	Fusarium
117	14.8	82.2	117750	13	ABD32653	ABD32653	Human can	C 190	14.4	77.8	616	14	ADZ91882	ADZ91882	Fusarium
118	14.4	80.0	201	13	ADS40630	ADS40630	Human aut	C 191	14.4	77.8	1317	4	ABL13055	ABL13055	Novel hum
119	14.4	80.0	364	3	AAE22364	AAE22364	Human sec	C 192	14.4	77.8	2298	12	ADQ63262	ADQ63262	DNA encod
120	14.4	80.0	367	8	ABE256573	ABE256573	Aspergill	C 193	14.4	77.8	2445	12	ADQ57280	ADQ57280	EGFR geno
121	14.4	80.0	380	13	ADRA61486	ADRA61486	Cotton CD	C 194	14.4	77.8	6274	4	ABL13054	ABL13054	Drosophill
122	14.4	80.0	419	5	ABX42529	ABX42529	Bovine ES	C 195	14.4	77.8	8979	3	AAF22305_03	AAF22305_03	Continuation (4 of
123	14.4	80.0	475	8	AAZ29846	AAZ29846	Human Lun	C 196	14.4	77.8	110000	6	ABBS5320_0	ABBS5320_0	Continuation (4 of
124	14.4	80.0	479	10	ADB33091	ADB33091	Human nov	C 197	14.4	77.8	110000	6	ABBS5320_3	ABBS5320_3	Continuation (4 of
125	14.4	80.0	479	6	ABL64293	ABL64293	Stomach c	C 198	14.4	77.8	110000	12	ADQ59398	ADQ59398	Human can
126	14.4	80.0	483	3	AAAC48139	AAAC48139	Zea maye	C 199	14.4	77.8	110000	14	ADZ13665_0	ADZ13665_0	Human can
127	14.4	80.0	498	3	AAK79223	AAK79223	Human imm	C 200	14.4	77.8	110000	14	ACF62741	ACF62741	Cancer ba
128	14.4	80.0	532	6	ABK90877	ABK90877	CDNA enco	C 201	14.4	77.8	189013	8	ADB20856	ADB20856	MRP1 base
129	14.4	80.0	564	8	ABE257962	ABE257962	Human sec	C 202	14.4	77.8	189013	10	ADB87945	ADB87945	Human UGT
130	14.4	80.0	581	8	ACD20381	ACD20381	DNA encod	C 203	14.4	77.8	189013	10	ADB86928	ADB86928	Human MDR
131	14.4	80.0	592	12	ACH73816	ACH73816	Human gen	C 204	14.4	77.8	189013	10	ADB82119	ADB82119	Human MDR
132	14.4	80.0	621	4	ABL25863	ABL25863	Drosophill	C 205	14.4	77.8	189013	6	ABN85584	ABN85584	Human EGF
133	14.4	80.0	636	5	ABV50466	ABV50466	Human pro	C 206	14.4	77.8	197496	13	ABD32854	ABD32854	Human can
134	14.4	80.0	658	3	AAE57768	AAE57768	Arachidon	C 207	14.4	77.8	209083	13	ADY35003	ADY35003	Murine CD
135	14.4	80.0	887	13	ADS10299	ADS10299	Human the	C 208	14.4	77.8	251364	13	ADY35005	ADY35005	Murine CD
136	14.4	80.0	939	3	AAE57769	AAE57769	Arachidon	C 209	14.4	77.8	251364	13	ADY34965	ADY34965	Murine CD
137	14.4	80.0	1022	2	AAZ11769	AAZ11769	Maize elo	C 210	14.4	77.8	341511	6	AAH55200	AAH55200	Genomic D
138	14.4	80.0	2136	13	ADM54721	ADM54721	Plant ful	C 211	14.4	77.8	349980	5	AAH41224	AAH41224	Pyrococ
139	14.4	80.0	2195	12	ABM67117	ABM67117	Murine ad	C 212	14.4	76.7	20	2	AAK96257	AAK96257	PCR prime
140	14.4	80.0	2621	4	ABL25862	ABL25862	Drosophill	C 213	13.8	76.7	25	9	ACT02856	ACT02856	Human mic
141	14.4	80.0	2754	3	AAE45843	AAE45843	Arabidops	C 214	13.8	76.7	25	2	AAV50875	AAV50875	Maize pol
142	14.4	80.0	2754	6	ABE13981	ABE13981	Arabidops	C 215	13.8	76.7	50	4	AAI78755	AAI78755	Human sil
143	14.4	80.0	2754	8	ADA68022	ADA68022	Arabidops	C 216	13.8	76.7	51	4	AAI78754	AAI78754	Human sil
144	14.4	80.0	2754	12	ADN72372	ADN72372	Thale cre	C 217	13.8	76.7	121	12	ADQ13249	ADQ13249	SNP target
145	14.4	80.0	3153	10	ADB62173	ADB62173	Human CDN	C 218	13.8	76.7	135	12	ADQ13249	ADQ13249	SNP target
146	14.4	80.0	4857	4	AAK80786	AAK80786	Human imm	C 219	13.8	76.7	147	14	ADY04873	ADY04873	Human imm
147	14.4	80.0	5122	4	AAK80784	AAK80784	Human imm	C 220	13.8	76.7	151	14	ABE85364	ABE85364	Human imm
148	14.4	80.0	5122	4	AAK80787	AAK80787	Human imm	C 221	13.8	76.7	165	6	ABK79320	ABK79320	Human imm
149	14.4	80.0	5122	4	AAK80785	AAK80785	Human imm	C 222	13.8	76.7	215	2	AAV89787	AAV89787	EST clone
150	14.4	80.0	6951	10	ADG32852	ADG32852	Human DNA	C 223	13.8	76.7	235	3	AAAC13109	AAAC13109	Human sec
151	14.4	80.0	6995	10	ADFS926	ADFS926	Human con	C 224	13.8	76.7	254	10	AD140326	AD140326	Human pur
152	14.4	80.0	7036	8	ABE257963	ABE257963	Human sec	C 225	13.8	76.7	262	4	AAK59014	AAK59014	Human imm
153	14.4	80.0	7376	4	AAK68043	AAK68043	Human imm	C 226	13.8	76.7	266	4	AAK74307	AAK74307	Human imm
154	14.4	80.0	7888	13	ADR83507	ADR83507	Human mul	C 227	13.8	76.7	266	4	AAK74306	AAK74306	Human imm
155	14.4	80.0	8323	2	AAO58700	AAO58700	LTR clone	C 228	13.8	76.7	266	4	AAK74305	AAK74305	Human imm
156	14.4	80.0	8323	2	AAO81042	AAO81042	Friend mu	C 229	13.8	76.7	302	4	AAI31590	AAI31590	Probe (BL
157	14.4	80.0	8323	2	AAAT80058	AAAT80058	LTR clone	C 230	13.8	76.7	304	4	AAK67036	AAK67036	Human imm
158	14.4	80.0	8323	2	AAZ07063	AAZ07063	Friend ec	C 231	13.8	76.7	304	4	AAK87033	AAK87033	Human imm
159	14.4	80.0	10367	2	AAQ58701	AAQ58701	PLRB332.	C 232	13.8	76.7	314	4	AAK72213	AAK72213	DNA encod
160	14.4	80.0	10367	2	AAAT80057	AAAT80057	Sequence	C 233	13.8	76.7	325	2	AAQ61119	AAQ61119	Human bra
161	14.4	80.0	10367	2	AAZ07067	AAZ07067	Glycopept	C 234	13.8	76.7	327	4	AAK61679	AAK61679	Human imm
162	14.4	80.0	18443	13	AAV83942	AAV83942	Bacterial	C 235	13.8	76.7	337	12	ADQ19132	ADQ19132	Human sof
163	14.4	80.0	19986	4	ADBS3481	ADBS3481	Human aut	C 236	13.8	76.7	343	4	AAK55228	AAK55228	Human imm
164	14.4	80.0	21429	4	AAE57362	AAE57362	Murine Cd	C 237	13.8	76.7	353	4	AAI14002	AAI14002	Probe #39
165	14.4	80.0	71953	11	ACN44552	ACN44552	Mouse gen	C 238	13.8	76.7	353	4	AAI14002	AAI14002	Probe #39

ALIGNMENTS

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DT 11-MAR-2004 (first entry)
XX Human kinase suppressor of Ras (KSR)-specific oligonucleotide.
DE
XX antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer;
XX pancreatic cancer; lung cancer; skin cancer; urinary tract cancer;
XX bladder cancer; liver cancer; thyroid cancer; colon cancer;
XX intestinal cancer; breast cancer; ovarian cancer; stomach cancer;
XX head cancer; neck cancer; oesophageal cancer; prostate cancer; leukaemia;
XX lymphoma; neuroblastoma; ss; human.
XX
XX Homo sapiens.
XX
XX WO2003101386-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US019661.
XX
XX 30-MAY-2002; 2002US-0384228P.
XX
XX 03-APR-2003; 2003US-0460023P.
XX
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
PA
XX Kolosnick RN, Xing HR;
XX
XX WPI; 2004-053335/05.
XX
XX New antisense oligonucleotides complementary to a region of Kinase
XX suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for
XX treating or inhibiting progression of cancer, e.g. pancreatic, lung,
XX skin, or bladder cancer.
XX
XX Example 2; SEQ ID NO 15; 120p; English.
XX
XX The invention comprises antisense oligonucleotides which are designed to
XX inhibit the expression of the kinase suppressor of Ras (KSR) gene. The
XX antisense oligonucleotides of the invention are useful for treating or
XX inhibiting the progression of cancer, such as: pancreatic cancer, lung
XX cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer,
XX thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian
XX cancer, stomach cancer, head and neck cancer, oesophageal cancer,
XX prostate cancer, leukaemia, lymphoma, and neuroblastoma. The present DNA
XX sequence represents a human KSR-specific oligonucleotide that was used in
XX an example of the invention.
XX
XX Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 18; DB 12; Length 18;
XX Best Local Similarity 100.0%; Pred. NO. 21;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 CGGACCTTAGAGGCAAG 18
XX |||||
XX 1 CGGACCTTAGAGGCAAG 18
XX
XX Db
XX
XX RESULT 2
XX ADG75391/c
XX ID ADG75391 standard; DNA; 18 BP.
XX
XX ADG75391;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human kinase suppressor of Ras (KSR) antisense oligonucleotide #3.
XX
XX antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer;
XX pancreatic cancer; lung cancer; skin cancer; urinary tract cancer;
XX bladder cancer; liver cancer; thyroid cancer; colon cancer;
XX intestinal cancer; breast cancer; ovarian cancer; stomach cancer;
XX head cancer; neck cancer; oesophageal cancer; prostate cancer; leukaemia;
XX lymphoma; neuroblastoma; ss; human.
XX

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XX OS Homo sapiens.
XX PN WO2003101386-A2.
XX PD 11-DEC-2003.
XX PF 29-MAY-2003; 2003WO-US016961.
XX PR 30-MAY-2002; 2002US-0384228P.
XX PR 03-APR-2003; 2003US-0460023P.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Kolesnick RN, Xing HR;
XX DR WPI; 2004-053335/05.
XX PT New antisense oligonucleotides complementary to a region of kinase
XX PT suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for
XX PT treating or inhibiting progression of cancer, e.g. pancreatic, lung,
XX PT skin, or bladder cancer.
XX PS Claim 8; SEQ ID NO 8; 120bp; English.
XX CC The invention comprises antisense oligonucleotides which are designed to
XX CC inhibit the expression of the kinase suppressor of Ras (KSR) gene. The
XX CC antisense oligonucleotides of the invention are useful for treating or
XX CC inhibiting the progression of cancer, such as: pancreatic cancer, lung
XX CC cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer,
XX CC thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian
XX CC cancer, stomach cancer, head and neck cancer, oesophageal cancer,
XX CC prostate cancer, leukaemia, lymphoma, and neuroblastoma. The present DNA
XX CC sequence represents a human KSR-specific antisense oligonucleotide of the
XX CC invention.
XX SQ Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 12; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 CGACCTTAGAGCAAG 18
XX Db 18 CGACCTTAGAGCAAG 1
XX
XX RESULT 3
XX AEA46548
XX ID AEA46548 standard; DNA; 18 BP.
XX AC AEA46548;
XX XX
XX 25-AUG-2005 (first entry)
XX DE Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:15.
XX XX
XX Kinase suppressor of Ras; KSR; cytosolic; neoplasm; pancreas tumor;
XX liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
XX gastrointestinal disease; respiratory disease; genitourinary disease;
XX endocrine disease; bladder tumor; colon tumor; intestine tumor;
XX head & neck tumor; leukemia; hematological disease; lymphoma;
XX immune disorder; esophagus tumor; breast tumor; stomach tumor;
XX nervous system tumor; neurological disease; ovary tumor;
XX gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
XX cardiovascular disease; antisense oligonucleotide; antisense therapy;
XX prostate tumor; andrology; cancer; hyperproliferation.
XX XX
XX Homo sapiens.
XX OS Mus sp.
XX OS Synthetic.
XX XX
XX PN WO2005056756-A2.

XX PD 23-JUN-2005.
XX XX
XX PF 03-DEC-2004; 2004WO-US040506.
XX XX
XX PR 03-DEC-2003; 2003US-00727358.
XX XX
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Kolesnick RN, Xing HR;
XX DR WPI; 2005-445165/45.
XX XX
XX PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
XX PT useful for inhibiting expression of mammalian KSR and treating
XX PT hyperproliferative conditions such as lung cancer, skin cancer, and
XX PT ovarian cancer.
XX PS Example 2; SEQ ID NO 15; 186bp; English.
XX CC The invention relates to an oligonucleotide (I) which is substantially
XX CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
XX CC the oligonucleotide inhibits the expression of KSR. Also included are the
XX CC following: an oligonucleotide (II) which is substantially complementary
XX CC to a translation initiation site, 5' untranslated region, coding region
XX CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
XX CC oligonucleotide (III) comprising a sequence substantially complementary
XX CC to the CA1 region of KSR; an antisense oligonucleotide (IV) comprising a
XX CC sequence substantially complementary to nucleotides 124-243 of the coding
XX CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
XX CC an antisense oligonucleotide (V) comprising a sequence chosen from
XX CC AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
XX CC comprising a nucleic acid sequence which encodes on transcription an
XX CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
XX CC (VII) transfected with (VI); an expression vector (VI) capable of
XX CC expressing a nucleic acid which is substantially complementary to the
XX CC coding sequence of KSR RNA, or its portion/fragment, where the
XX CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
XX CC expression vector (V2) capable of expressing an oligonucleotide which is
XX CC substantially complementary to the CA1 region of the coding sequence of
XX CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
XX CC expression of KSR; a pharmaceutical composition (PCI) comprising (I) and
XX CC a carrier or diluent; a composition (CI) comprising (I) and a carrier or
XX CC diluent; a composition (C2) comprising one or more chemotherapeutic or
XX CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
XX CC encoding mammalian KSR and which inhibits KSR expression; a composition
XX CC (C3) comprising an expression vector and a carrier or diluent, where the
XX CC expression vector is capable of expressing nucleic acid which is
XX CC substantially complementary to the coding sequence of KSR RNA, or its
XX CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
XX CC inhibiting (M1) the expression of mammalian KSR comprising contacting
XX CC cells which express KSR with a nucleic acid which is complementary to a
XX CC portion of the mRNA encoding KSR; treating or preventing (M2) a
XX CC hyperproliferative condition associated with the expression of gf-Ras or
XX CC heightened expression of Ras in a mammal comprising administering to the
XX CC mammal a compound or agent which inhibits the expression of mammalian KSR
XX CC protein; treating or preventing (M3) a hyperproliferative condition
XX CC associated with the expression of gf-Ras or heightened expression of Ras
XX CC in a mammal comprising expressing in the mammal or administering to the
XX CC mammal therapeutically effective amount of a nucleic acid which is
XX CC complementary to a portion of the mRNA encoding KSR; treating or
XX CC inhibiting (M4) the progression of cancer in a mammal comprising
XX CC administering to a mammal a compound or agent which inhibits the
XX CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
XX CC cells in a mammal, by administering to a mammal a compound or agent which
XX CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
XX CC VEGF expression or activity in a mammal, by administering a compound or
XX CC agent that inhibits the expression of mammalian KSR protein; stimulating
XX CC angiogenesis in a mammal comprising administering to a mammal a
XX CC therapeutically effective amount of a compound or agent which activates
XX CC the expression of mammalian KSR protein or a vector expressing mammalian
XX CC KSR; identifying compounds or agents which inhibit the expression of KSR,
XX CC by incubating a cell expressing KSR in the presence and absence of a

CC candidate compound or agent, and detecting or measuring the expression of
 CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) is useful
 CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from
 CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents a KSR antisense oligonucleotide.
 XX
 SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pired. No. 21;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CGGACCTAGAGCGCAAG 18
 1 CGGACCTAGAGCGCAAG 18
 Db
 RESULT 4
 AEA46538
 ID AEA46538 standard; DNA; 18 BP.
 XX
 AC AEA46538;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:5.
 XX
 KW Kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor;
 KW liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
 KW gastrointestinal disease; respiratory disease; genitourinary disease;
 KW endocrine disease; bladder tumor; colon tumor; intestine tumor;
 KW head & neck tumor; leukemia; hematological disease; lymphoma;
 KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense oligonucleotide; antisense therapy;
 KW prostate tumor; andrology; cancer; hyperproliferation.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS
 PN MO2005056756-A2.
 XX
 PD 23-JUN-2005.
 XX
 PF 03-DEC-2004; 2004MO-US040506.
 XX
 PR 03-DEC-2003; 2003US-00727358.
 XX
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PA Kolesnick RN, Xing HR;
 PI
 XX
 DR WPI; 2005-445165/45.
 XX
 PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 useful for inhibiting expression of mammalian KSR and treating

PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 XX
 PS Claim 7; SEQ ID NO 5; 186pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the CAl region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AEA46539, AEA46540 and AEA46541, and; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription; a cell
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (V2) capable of expressing an oligonucleotide which is
 CC substantially complementary to the CAl region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (PC1) comprising (I) and
 CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
 CC diluent; a composition (C2) comprising one or more chemotherapeutic or
 CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
 CC inhibiting (M1) the expression of mammalian KSR comprising contacting
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; treating or preventing (M3) a hyperproliferative condition
 CC associated with the expression of gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the
 CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 CC cells in a mammal, by administering to a mammal a compound or agent which
 CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
 CC VEGF expression or activity in a mammal, by administering a compound or
 CC agent that inhibits the expression of mammalian KSR protein; stimulating
 CC angiogenesis in a mammal comprising administering to a mammal a
 CC therapeutically effective amount of a compound or agent which activates
 CC the expression of mammalian KSR protein or a vector expressing mammalian
 CC KSR; identifying compounds or agents which inhibit the expression of KSR,
 CC by incubating a cell expressing KSR in the presence and absence of a
 CC candidate compound or agent, and detecting or measuring the expression of
 CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) is useful
 CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from

CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents a KSR antisense oligonucleotide.
 XX
 SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGACCTAGAGGCAAG 18
 DB 1 CGGACCTAGAGGCAAG 18
 RESULT 5
 AEA46561/c
 ID AEA46561 standard; DNA; 18 BP.
 XX
 AC AEA46561;
 DT 25-AUG-2005 (first entry)
 XX
 DE Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:28.
 XX
 KW Kinase suppressor of Ras; KSR; cytosolic; neoplasm; pancreas tumor;
 KW liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
 KW gastrointestinal disease; respiratory disease; genitourinary disease;
 KW endocrine disease; bladder tumor; colon tumor; intestine tumor;
 KW head & neck tumor; leukemia; hematological disease; lymphoma;
 KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; angiogenic;
 KW cardiovascular disease; antisense oligonucleotide; antisense therapy;
 KW prostate tumor; andrology; cancer; hyperproliferation.
 XX
 OS Homo sapiens.
 OS Syn sp.
 OS Synthetic.
 XX
 PN WO2005056756-A2.
 XX
 PD 23-JUN-2005.
 XX
 PF 03-DEC-2004; 2004WO-US040506.
 XX
 PR 03-DEC-2003; 2003US-00727358.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Kolesnick RN, Xing HR;
 DR WPI; 2005-445165/45.
 XX
 PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 XX
 PS Claim 8; SEQ ID NO 28; 186pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the 3' region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;

CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (V2) capable of expressing an oligonucleotide which is
 CC substantially complementary to the 3' region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (PC1) comprising (I) and
 CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
 CC diluent; a composition (C2) comprising one or more chemotherapeutic or
 CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
 CC inhibiting (M1) the expression of mammalian KSR comprising contacting
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; treating or preventing (M3) a hyperproliferative condition
 CC associated with the expression of gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the
 CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 CC cells in a mammal, by administering to a mammal a compound or agent which
 CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
 CC VEGF expression or activity in a mammal, by administering a compound or
 CC agent that inhibits the expression of mammalian KSR protein; stimulating
 CC angiogenesis in a mammal comprising administering to a mammal a
 CC therapeutically effective amount of a compound or agent which activates
 CC the expression of mammalian KSR protein or a vector expressing mammalian
 CC KSR; identifying compounds or agents which inhibit the expression of KSR,
 CC by incubating a cell expressing KSR in the presence and absence of a
 CC candidate compound or agent, and detecting or measuring the expression of
 CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) is useful
 CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from
 CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents a KSR antisense oligonucleotide.
 XX
 SQ Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGACCTAGAGGCAAG 18
 DB 1 CGGACCTAGAGGCAAG 1

RESULT 6
AEA46534
ID AEA46534 standard; DNA; 120 BP.
XX
XX AEA46534;
AC
XX 25-AUG-2005 (first entry)
XX
XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:1.
XX
XX Kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor;
XX liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
XX gastrointestinal disease; respiratory disease; genitourinary disease;
XX endocrine disease; bladder tumor; colon tumor; intestine tumor;
XX head & neck tumor; leukemia; hematological disease; lymphoma;
XX immune disorder; esophagus tumor; breast tumor; stomach tumor;
XX nervous system tumor; neurological disease; ovary tumor;
XX gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
XX cardiovascular disease; antisense oligonucleotide; antisense therapy;
XX prostate tumor; andrology; cancer; hyperproliferation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1. 120
FT /tag= a
FT /partial
FT /product= "Kinase suppressor of Ras (KSR) CA1 domain"
FT /note= "No start or stop codon shown"
XX
XX MO2005056756-A2.
XX
XX 23-JUN-2005.
XX
XX 03-DEC-2004; 2004MO-US040506.
XX
XX 03-DEC-2003; 2003US-00727358.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Kolesnick RN, Xing HR;
XX
XX WPI; 2005-445165/45.
XX
XX P-PSDB; AEA46535.
XX
XX New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
XX useful for inhibiting expression of mammalian KSR and treating
XX hyperproliferative conditions such as lung cancer, skin cancer, and
XX ovarian cancer.
XX
XX Claim 6; SEQ ID NO:1; 186bp; English.
XX
XX The invention relates to an oligonucleotide (I) which is substantially
XX complementary to a region of kinase suppressor of Ras (KSR) RNA, where
XX the oligonucleotide inhibits the expression of KSR. Also included are the
XX following: an oligonucleotide (II) which is substantially complementary
XX to a translation initiation site, 5' untranslated region, coding region
XX or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
XX oligonucleotide (III) comprising a sequence substantially complementary
XX to the CA1 region of KSR; an antisense oligonucleotide (IV) comprising a
XX sequence substantially complementary to nucleotides 124-243 of the coding
XX sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
XX an antisense oligonucleotide (V) comprising a sequence chosen from
XX AEA46539, AEA46540 and AEA46541, and ; a recombinant DNA molecule (VI)
XX comprising a nucleic acid sequence which encodes or transcribes an
XX antisense RNA complementary to mammalian KSR RNA or its portion; a cell
XX (VII) transfected with (VI); an expression vector (VI) capable of
XX expressing a nucleic acid which is substantially complementary to the
XX coding sequence of KSR RNA, or its portion/fragment, where the
XX oligonucleotide/nucleic acid inhibits the expression of KSR; an
XX expression vector (V2) capable of expressing an oligonucleotide which is

CC substantially complementary to the CA1 region of the coding sequence of
CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
CC expression of KSR; a pharmaceutical composition (PCI) comprising (I) and
CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
CC diluent; a composition (C2) comprising one or more chemotherapeutic or
CC radiotherapeutic agent and an oligonucleotide which is targeted to a RNA
CC encoding mammalian KSR and which inhibits KSR expression; a composition
CC (C3) comprising an expression vector and a carrier or diluent, where the
CC expression vector is capable of expressing nucleic acid which is
CC substantially complementary to the coding sequence of KSR RNA, or its
CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
CC inhibiting (M1) the expression of mammalian KSR comprising contacting
CC cells which express KSR with a nucleic acid which is complementary to a
CC portion of the mRNA encoding KSR; treating or preventing (M2) a
CC hyperproliferative condition associated with the expression of gf-Ras or
CC heightened expression of Ras in a mammal comprising administering to the
CC mammal a compound or agent which inhibits the expression of mammalian KSR
CC protein, treating or preventing (M3) a hyperproliferative condition
CC associated with the expression of gf-Ras or heightened expression of Ras
CC in a mammal comprising expressing in the mammal or administering to the
CC mammal therapeutically effective amount of a nucleic acid which is
CC complementary to a portion of the mRNA encoding KSR; treating or
CC inhibiting (M4) the progression of cancer in a mammal comprising
CC administering to a mammal a compound or agent which inhibits the
CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
CC cells in a mammal, by administering to a mammal a compound or agent which
CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
CC VEGF expression or activity in a mammal, by administering a compound or
CC agent that inhibits the expression of mammalian KSR protein; stimulating
CC angiogenesis in a mammal comprising administering to a mammal a
CC therapeutically effective amount of a compound or agent which activates
CC the expression of mammalian KSR protein or a vector expressing mammalian
CC KSR; identifying compounds or agents which inhibit the expression of KSR,
CC by incubating a cell expressing KSR in the presence and absence of a
CC candidate compound or agent, and detecting or measuring the expression of
CC KSR in the presence and absence of a candidate compound or agent, where a
CC decrease in the expression of KSR in the presence of the candidate
CC compound or agent versus in the absence of the candidate compound or
CC agent indicates that the compound or agent inhibits the expression of KSR
CC ; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the
CC expression of mammalian KSR comprising contacting cells which express KSR
CC with (I), where expression of mammalian KSR is inhibited. (I) Is useful
CC for conferring radioresistance to ionizing radiation in tumor cells in a
CC mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is
CC useful for inhibiting or reducing VEGF expression or activity in a
CC mammal. The methods are useful for treating or preventing
CC hyperproliferative condition associated with expression of gf-Ras or
CC heightened expression of Ras in a mammal and for treating or inhibiting
CC the progression of cancer in a mammal. The cancer is chosen from
CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC cancer. The present sequence represents a KSR antisense oligonucleotide.
XX
XX Sequence 120 BP; 31 A; 36 C; 32 G; 21 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 14; Length 120;
XX Best Local Similarity 100.0%; Pred. No. 22;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CGAGCCTTGAAGCAAAAG 18
XX |||||
XX Db 91 CGAGCCTTGAAGCAAAAG 108
XX |||||
XX
XX RESULT 7
XX AEA46558
XX ID AEA46558 standard; DNA; 121 BP.
XX
XX AEA46558;
XX
XX 25-AUG-2005 (first entry)

DE	Kinase. suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:25.	
XX		
KW	Kinase suppressor of Ras; KSR; cytosolic; neoplasm; pancreas tumor;	
KW	liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;	
KW	gastrointestinal disease; respiratory disease; genitourinary disease;	
KW	endocrine disease; bladder tumor; colon tumor; intestine tumor;	
KW	head & neck tumor; leukemia; hematological disease; lymphoma;	
KW	immune disorder; esophagus tumor; breast tumor; stomach tumor;	
KW	neovous system tumor; neurological disease; ovary tumor;	
KW	gynecologic and obstetrics; ss; angiogenesis disorder; antiangiogenic;	
KW	cardiovascular disease; antisense oligonucleotide; antisense therapy;	
KW	prostate tumor; andrology; cancer; hyperproliferation.	
XX		
OS	Homo sapiens.	
OS	Mus sp.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..120
FT		/*tag=
FT		/partial
FT		/product= "Kinase suppressor of Ras (KSR) fragment"
FT		/note= "No start or stop codon shown"
XX		
PN	WO2005056756-A2.	
XX		
PD	23-JUN-2005.	
XX		
XX	03-DEC-2004; 2004WO-US040506.	
PF	03-DEC-2003; 2003US-00727358.	
PR		
XX		
PA	(SLOK) SLOAN KETTERING INST CANCER RES.	
XX		
PI	Kolesnck RN, Xing HR;	
XX		
DR	WPI: 2005-445165/45.	
XX	P-PSDB; AEA46559.	
XX		
PT	New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,	
PT	useful for inhibiting expression of mammalian KSR and treating	
PT	hyperproliferative conditions such as lung cancer, skin cancer, and	
PT	ovarian cancer.	
XX		
PS	Claim 6; SEQ ID NO 25; 186bp; English.	
XX		
CC	The invention relates to an oligonucleotide (I) which is substantially	
CC	complementary to a region of kinase suppressor of Ras (KSR) RNA, where	
CC	the oligonucleotide inhibits the expression of KSR. Also included are the	
CC	following: an oligonucleotide (II) which is substantially complementary	
CC	to a translation initiation site, 5' untranslated region, coding region	
CC	or 3' untranslated region of mRNA encoding mammalian KSR; an antisense	
CC	oligonucleotide (III) comprising a sequence substantially complementary	
CC	to the 3' untranslated region of KSR; an antisense oligonucleotide (IV) comprising a	
CC	sequence substantially complementary to nucleotides 124-243 of the coding	
CC	sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;	
CC	an antisense oligonucleotide (V) comprising a sequence chosen from	
CC	AEA46539, AEA46540 and AEA46541, and; a recombinant DNA molecule (VI)	
CC	comprising a nucleic acid sequence which encodes on transcription an	
CC	antisense RNA complementary to mammalian KSR RNA or its portion; a cell	
CC	(VII) transfected with (VI); an expression vector (VI) capable of	
CC	expressing a nucleic acid which is substantially complementary to the	
CC	coding sequence of KSR RNA, or its portion/fragment, where the	
CC	oligonucleotide/nucleic acid inhibits the expression of KSR; an	
CC	expression vector (VII) capable of expressing an oligonucleotide which is	
CC	substantially complementary to the 3' untranslated region of the coding sequence of	
CC	KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the	
CC	expression of KSR; a pharmaceutical composition (PCI) comprising (I) and	
CC	a carrier or diluent; a composition (CI) comprising (I) and a carrier or	
CC	diluent; a composition (C2) comprising one or more chemotherapeutic or	
CC	radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA	
CC	encoding mammalian KSR and which inhibits KSR expression; a composition	

CC	(C3) comprising an expression vector and a carrier or diluent, where the
CC	expression vector is capable of expressing nucleic acid which is
CC	substantially complementary to the coding sequence of KSR RNA, or its
CC	portion/fragment, where the nucleic acid inhibits the expression of KSR;
CC	inhibiting (M1) the expression of mammalian KSR comprising contacting
CC	cells which express KSR with a nucleic acid which is complementary to a
CC	portion of the mRNA encoding KSR; treating or preventing (M2) a
CC	hyperproliferative condition associated with the expression of gf-Ras or
CC	heightened expression of Ras in a mammal comprising administering to the
CC	mammal a compound or agent which inhibits the expression of mammalian KSR
CC	protein; treating or preventing (M3) a hyperproliferative condition
CC	associated with the expression of gf-Ras or heightened expression of Ras
CC	in a mammal comprising expressing in the mammal or administering to the
CC	mammal therapeutically effective amount of a nucleic acid which is
CC	complementary to a portion of the mRNA encoding KSR; treating or
CC	inhibiting (M4) the progression of cancer in a mammal comprising
CC	administering to a mammal a compound or agent which inhibits the
CC	expression of mammalian KSR protein; inhibiting angiogenesis of tumor
CC	cells in a mammal, by administering to a mammal a compound or agent which
CC	inhibits the expression of mammalian KSR protein; inhibiting or reducing
CC	VEGF expression or activity in a mammal, by administering a compound or
CC	agent that inhibits the expression of mammalian KSR protein; stimulating
CC	angiogenesis in a mammal comprising administering to a mammal a
CC	therapeutically effective amount of a compound or agent which activates
CC	the expression of mammalian KSR protein or a vector expressing mammalian
CC	KSR; identifying compounds or agents which inhibit the expression of KSR,
CC	by incubating a cell expressing KSR in the presence and absence of a
CC	candidate compound or agent, and detecting or measuring the expression of
CC	KSR in the presence and absence of a candidate compound or agent, where a
CC	compound or agent versus in the presence of the candidate
CC	compound or agent indicates that the compound or agent inhibits the expression of KSR
CC	; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the
CC	expression of mammalian KSR comprising contacting cells which express KSR
CC	with (I), where expression of mammalian KSR is inhibited. (I) is useful
CC	for conferring radiosensitivity to ionizing radiation in tumor cells in a
CC	mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is
CC	useful for inhibiting or reducing VEGF expression or activity in a
CC	mammal. The methods are useful for treating or preventing
CC	hyperproliferative condition associated with expression of gf-Ras or
CC	heightened expression of Ras in a mammal and for treating or inhibiting
CC	the progression of cancer in a mammal. The cancer is chosen from
CC	pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC	bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC	cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
CC	cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC	cancer. The present sequence represents a KSR antisense oligonucleotide.
XX	
SO	Sequence 121 BP; 29 A; 40 C; 32 G; 20 T; 0 U; 0 Other;
	Query Match 100.0%; Score 18; DB 14; Length 121;
	Best Local Similarity 100.0%; Pred. No. 22;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGGACCTAGAGCGAAG 18
DB	91 CGGACCTAGAGCGAAG 108
RESULT 8	
AEA46557	
ID	AEA46557 standard; cDNA; 2601 BP.
XX	
AC	AEA46557;
XX	
DT	25-AUG-2005 (first entry)
XX	
DB	Human kinase suppressor of Ras 1 (KSR1) cDNA.
XX	
KW	gene; Kinase suppressor of Ras; KSR; cytosol; neoplasm;
KW	pancreas tumor; liver tumor; skin tumor; thyroid tumor; lung tumor;
KW	urinary tract tumor; gastrointestinal disease; respiratory disease;
KW	genitourinary disease; endocrine disease; bladder tumor; colon tumor;

KW Intestine tumor; head & neck tumor; leukemia; hematological disease;
 KW lymphoma; immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecologic and obstetric; se; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense therapy; prostate tumor; andrology;
 KW cancer; hyperproliferation.
 XX
 XX Homo sapiens.
 OS
 PN WO2005056756-A2.
 XX
 PD 23-JUN-2005.
 XX
 PE 03-DEC-2004; 2004MO-US040506.
 XX
 PR 03-DEC-2003; 2003JUS-00727358.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI koleencik RN, Xing HR;
 DR MPI; 2005-445165/45.
 XX
 PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 PS
 PS Example 5; SEQ ID NO 24; 186pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the CA1 region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC ABA46539, ABA46540 and ABA46541, and; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (V2) capable of expressing an oligonucleotide which is
 CC substantially complementary to the CA1 region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (Pc1) comprising (I) and
 CC a carrier or diluent; a composition (C1) comprising (I) and a carrier or
 CC diluent; a composition (C2) comprising one or more chemotherapeutic or
 CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR;
 CC inhibiting (M1) the expression of mammalian KSR comprising contacting
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; treating or preventing (M3) a hyperproliferative condition
 CC associated with the expression of gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the

CC	expression of mammalian KSR protein; inhibiting angiogenesis of tumor
CC	cells in a mammal, by administering to a mammal a compound or agent which
CC	inhibits the expression of mammalian KSR protein; inhibiting or reducing
CC	VEGF expression or activity in a mammal, by administering a compound or
CC	agent that inhibits the expression of mammalian KSR protein; stimulating
CC	angiogenesis in a mammal comprising administering to a mammal a
CC	therapeutically effective amount of a compound or agent which activates
CC	the expression of mammalian KSR protein or a vector expressing mammalian
CC	KSR; identifying compounds or agents which inhibit the expression of KSR,
CC	by incubating a cell expressing KSR in the presence and absence of a
CC	candidate compound or agent, and detecting or measuring the expression of
CC	KSR in the presence and absence of a candidate compound or agent, where a
CC	decrease in the expression of KSR in the presence of the candidate
CC	compound or agent versus in the absence of the candidate compound or
CC	agent indicates that the compound or agent inhibits the expression of KSR
CC	; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the
CC	expression of mammalian KSR comprising contacting cells which express KSR
CC	with (I), where expression of mammalian KSR is inhibited. (I) Is useful
CC	for conferring radiosensitivity to ionizing radiation in tumor cells in a
CC	mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is
CC	useful for inhibiting or reducing VEGF expression or activity in a
CC	mammal. The methods are useful for treating or preventing
CC	hyperproliferative condition associated with expression of gf-Ras or
CC	heightened expression of Ras in a mammal and for treating or inhibiting
CC	the progression of cancer in a mammal. The cancer is chosen from
CC	pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
CC	bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
CC	cancer, leukemias, lymphomas, neuroblastoma, head and neck cancer, breast
CC	cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
CC	cancer. The present sequence represents human .KSR1 cDNA.
SQ	
XQ	Sequence 2601 BP; 565 A; 818 C; 772 G; 446 T; 0 U; 0 Other;
Query Match	100.0%; Score 18; DB 14; Length 2601;
Best Local Similarity	100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dy	1 CGGACCTTAGAGCGAAG 18 Db 187 CGGACCTTAGAGCGAAG 204
RESULT 9	
AEA46544	ID AEA46544 standard; cDNA; 4034 BP.
XX	AEA46544;
AC	25-AUG-2005 (first entry)
DT	Mouse kinase suppressor of Ras (KSR) cDNA.
XX	
DE	gene; Kinase suppressor of Ras; KSR, cytosstatic; neoplasm;
KM	pancreas tumor; liver tumor; skin tumor; thyroid tumor; lung tumor;
KM	urinary tract tumor; gastrointestinal disease; respiratory disease;
KM	genitourinary disease; endocrine disease; bladder tumor; colon tumor;
KM	intestinal tumor; head & neck tumor; leukemia; hematological disease;
KM	lymphoma; immune disorder; esophagus tumor; breast tumor; stomach tumor;
KM	nervous system tumor; neurological disease; ovary tumor;
KM	gynecologic and obstetric; se; angiogenesis disorder; antiangiogenic;
KM	cardiovascular disease; antitense therapy; prostate tumor; andrology;
KM	cancer; hyperproliferation.
XX	
XS	Mus sp.
OS	
FH	Key Location/Qualifiers
FT	CDS 83..2704
FT	/tag= a
XX	/product= "Mouse kinase suppressor of Ras (KSR)"
PN	W02005056756-A2.
XX	
JD	23-JUN-2005.

XX 03-DEC-2004; 2004MO-US040506.
 XX 03-DEC-2003; 2003US-00727358.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Kolesnick RN, Xing HR;
 XX MPI; 2005-445165/45.
 XX P-PSDB; AEA46542.
 XX
 XX New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 XX useful for inhibiting expression of mammalian KSR and treating
 XX hyperproliferative conditions such as lung cancer, skin cancer, and
 XX ovarian cancer.
 XX
 XX Disclosure; SEQ ID NO 11; 186pp; English.
 XX
 XX The invention relates to an oligonucleotide (I) which is substantially
 XX complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 XX the oligonucleotide inhibits the expression of KSR. Also included are the
 XX following: an oligonucleotide (II) which is substantially complementary
 XX to a translation initiation site, 5' untranslated region, coding region
 XX or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 XX oligonucleotide (III) comprising a sequence substantially complementary
 XX to the CAl region of KSR; an antisense oligonucleotide (IV) comprising a
 XX sequence substantially complementary to nucleotides 124-243 of the coding
 XX sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 XX an antisense oligonucleotide (V) comprising a sequence chosen from
 XX AEA46539, AEA46540 and AEA46541, and; a recombinant DNA molecule (VI)
 XX comprising a nucleic acid sequence which encodes on transcription an
 XX antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 XX (VII) transfected with (VI); an expression vector (VI) capable of
 XX expressing a nucleic acid which is substantially complementary to the
 XX coding sequence of KSR RNA, or its portion/fragment, where the
 XX oligonucleotide/nucleic acid inhibits the expression of KSR; an
 XX expression vector (V2) capable of expressing an oligonucleotide which is
 XX substantially complementary to the CAl region of the coding sequence of
 XX KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 XX expression of KSR; a pharmaceutical composition (PC1) comprising (I) and
 XX a carrier or diluent; a composition (C1) comprising (I) and a carrier or
 XX diluent; a composition (C2) comprising one or more chemotherapeutic or
 XX radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 XX encoding mammalian KSR and which inhibits KSR expression; a composition
 XX (C3) comprising an expression vector and a carrier or diluent, where the
 XX expression vector is capable of expressing nucleic acid which is
 XX substantially complementary to the coding sequence of KSR RNA, or its
 XX portion/fragment, where the nucleic acid inhibits the expression of KSR;
 XX inhibiting (M1) the expression of mammalian KSR comprising contacting
 XX cells which express KSR with a nucleic acid which is complementary to a
 XX portion of the mRNA encoding KSR; treating or preventing (M2) a
 XX hyperproliferative condition associated with the expression of gf-Ras or
 XX heightened expression of Ras in a mammal comprising administering to the
 XX mammal a compound or agent which inhibits the expression of mammalian KSR
 XX protein; treating or preventing (M3) a hyperproliferative condition
 XX associated with the expression of gf-Ras or heightened expression of Ras
 XX in a mammal comprising expressing in the mammal or administering to the
 XX mammal therapeutically effective amount of a nucleic acid which is
 XX complementary to a portion of the mRNA encoding KSR; treating or
 XX inhibiting (M4) the progression of cancer in a mammal comprising
 XX administering to a mammal a compound or agent which inhibits the
 XX expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 XX cells in a mammal, by administering to a mammal a compound or agent which
 XX inhibits the expression of mammalian KSR protein; inhibiting or reducing
 XX VEGF expression or activity in a mammal, by administering a compound or
 XX agent that inhibits the expression of mammalian KSR protein; stimulating
 XX angiogenesis in a mammal comprising administering to a mammal a
 XX therapeutically effective amount of a compound or agent which activates
 XX the expression of mammalian KSR protein or a vector expressing mammalian
 XX KSR; identifying compounds or agents which inhibit the expression of KSR,
 XX by incubating a cell expressing KSR in the presence and absence of a
 XX candidate compound or agent, and detecting or measuring the expression of

CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) Is useful
 CC for conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from
 CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents mouse KSR cDNA.
 XX
 XX Sequence 4034 BP; 906 A; 1200 C; 1171 G; 757 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 18; DB 14; Length 4034;
 XX Best Local Similarity 100.0%; Pred. No. 25;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 CGGACCTTAGGCGCAAG 18
 XX |||||
 XX 296 CGGACCTTAGGCGCAAG 313
 XX
 XX
 XX RESULT 10
 XX AAT72155
 XX ID AAT72155 standard; cDNA; 4094 BP.
 XX AC AAT72155;
 XX DT 13-SEP-1997 (first entry)
 XX DE Mouse Ksr-1 (Kinase suppressor of Ras) cDNA.
 XX KM Kinase suppressor of Ras; Ksr-1; signal transduction; cell growth;
 XX cell differentiation; gene therapy; diagnosis; de.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 XX FT CDS 83..2704
 XX /*tag= a
 XX
 XX PN W09721820-A2.
 XX PD 19-JUN-1997.
 XX PR 13-DEC-1996; 96MO-US019941.
 XX PA 13-DEC-1995; 95US-00571758.
 XX (REGC) UNIV CALIFORNIA.
 XX PI Rubin G, Therrien M, Chang H, Karim F, Waasatman D;
 XX MPI; 1997-332791/30.
 XX DR P-PSDB; AAW19918.
 XX PT Isolated kinase suppressor of ras protein - used to identify lead
 XX compounds and in diagnosis or treatment of disease associated with Ksr
 XX activity or Ksr signal transduction.
 XX PS Claim 5; Page 32-34; 49pp; English.
 XX A cDNA clone (AAT72155) includes a complete open reading frame that codes
 XX for mouse kinase suppressor of Ras (AAW19918) designated Ksr-1, a novel

CC protein kinase involved in the regulation of cell growth and
 CC differentiation. It was isolated from a mouse PC4 teratocarcinoma cell
 CC line with a probe corresponding to hb, a sequence that had been
 CC identified as showing similarity to Drosophila melanogaster Ksr (see also
 CC AAT72153). Drosophila virilis and human Ksr sequences (see also AAT72154,
 CC AAT82156-57) have also been identified. These Ksr homologues define a
 CC novel class of kinases related to raf kinases. Ksr nucleic acids can be
 CC used to produce Ksr polypeptides, as probes to identify mutant Ksr
 CC alleles associated with disease, and in gene therapy applications
 CC
 XX Sequence 4094 BP; 924 A; 1212 C; 1193 G; 765 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 4094;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGACCTTAGAGGCAAG 18
 DB 296 CGGACCTTAGAGGCAAG 313

RESULT 11

ADG75394
 ID ADG75394 standard; cDNA; 4094 BP.

XX ADG75394;

DT 11-MAR-2004 (first entry)

XX Mouse kinase suppressor of Ras (KSR) coding sequence.

XX antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer;
 KW pancreatic cancer; lung cancer; skin cancer; urinary tract cancer;
 KW bladder cancer; liver cancer; thyroid cancer; colon cancer;
 KW intestinal cancer; breast cancer; ovarian cancer; stomach cancer;
 KW head cancer; neck cancer; oesophageal cancer; prostate cancer; leukaemia;
 KW lymphoma; neuroblastoma; mouse; murine; gene; ss.

XX Mus sp.

PN MO2003101386-A2.

XX 11-DEC-2003.

PF 29-MAY-2003; 2003WO-US016961.

PR 30-MAY-2002; 2002US-0384228P.

PR 03-APR-2003; 2003US-0460023P.

(SLOK) SLOAN KETTERING INST CANCER RES.

XX Kolesnick RN, Xing HR;

XX WPI; 2004-053335/05.

DR P-PSDB; ADG75392.

XX New antisense oligonucleotides complementary to a region of kinase
 PT suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for
 PT treating or inhibiting progression of cancer, e.g. pancreatic, lung,
 PT skin, or bladder cancer.

XX Example 1; SEQ ID NO 11; 120bp; English.

XX The invention comprises antisense oligonucleotides which are designed to
 CC inhibit the expression of the kinase suppressor of Ras (KSR) gene. The
 CC antisense oligonucleotides of the invention are useful for treating or
 CC inhibiting the progression of cancer, such as: pancreatic cancer, lung
 CC cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer,
 CC thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian
 CC cancer, stomach cancer, head and neck cancer, oesophageal cancer,
 CC prostate cancer, leukaemia, lymphoma, and neuroblastoma. The present cDNA
 CC sequence encodes the mouse KSR protein.

SQ Sequence 4094 BP; 924 A; 1212 C; 1193 G; 765 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 4094;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGACCTTAGAGGCAAG 18
 DB 296 CGGACCTTAGAGGCAAG 313

RESULT 12

AEA46541/C
 ID AEA46541 standard; DNA; 16 BP.

XX AEA46541;

DT 25-AUG-2005 (first entry)

XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:8.

XX liver tumor; skin tumor; thyroid tumor; lung tumor; pancreas tumor;
 KW gastrointestinal disease; respiratory disease; genitourinary disease;
 KW endocrine disease; bladder tumor; colon tumor; intestine tumor;
 KW head & neck tumor; leukemia; hematological disease; lymphoma;
 KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense oligonucleotide; antisense therapy;
 KW prostate tumor; andrology; cancer; hyperproliferation.

XX Homo sapiens.

OS Mus sp.

PN WO2005056756-A2.

XX 23-JUN-2005.

PF 03-DEC-2004; 2004WO-US040506.

PR 03-DEC-2003; 2003US-00727358.

(SLOK) SLOAN KETTERING INST CANCER RES.

XX Kolesnick RN, Xing HR;

XX WPI; 2005-445165/45.

XX New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.

XX Claim 8; SEQ ID NO 8; 186bp; English.

XX The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation/initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the 3'UTR region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AEA46539, AEA46540 and AEA46541, and; a recombinant DNA molecule (VI)
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VI) capable of
 CC expressing a nucleic acid which is substantially complementary to the

XX Leukemia-related DNA sequence #1342.
DE Cytostatic; Gene therapy; Leukemia; ss.
XX
XX Unidentified.
OS
XX WO2003039443-A2.
FN
XX
XX 15-MAY-2003.
PD
XX
XX 04-NOV-2002; 2002WO-EP012303.
PF
XX 05-NOV-2001; 2001EP-00126244.
PR
XX 30-APR-2002; 2002EP-00009758.
PR
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
XX
XX Haferlach T, Schoch C, Kern W, Kohlmann A, Schittger S, Dugas M;
PI Eils R, Brose B, Mergenthaler S;
XX WPI; 2003-505037/47.
DR
XX Determining the subtype of leukemia cells and whether a patient sample
PT contains leukemia cells or other cells, useful for treating leukemia,
PT comprises determining the expression profile of a group of markers in a
PT patient sample.
XX
XX Disclosure; SEQ ID NO 1342; 2938bp; English.
PS
XX The present invention relates to a method (M1) for determining the
CC subtype of leukemia cells and whether a patient sample contains
CC leukemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukemia.
XX
XX Sequence 388 BP; 119 A; 91 C; 57 G; 121 T; 0 U; 0 Other;
SQ
Query Match 85.6%; Score 15.4; DB 10; Length 388;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGAGGCAAG 18
DB 360 GGACCTAGAGGCAAG 344
RESULT 16
AAK88398/C
ID AAK88398 standard; cDNA; 514 BP.
XX
XX AAK88398;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX Human digestive system antigen coding sequence SEQ ID NO: 714.
DE
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ss.
XX
XX Homo sapiens.
OS
XX WO200155314-A2.
FN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US001324.
PF

XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-022681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
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PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251888P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251899P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
FI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-502630/55.
DR P-FSDB; AAM92625.
XX
PT Polynucleotides encoding digestive system antigens, useful for

PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
XX Claim 1; SEQ ID NO 714; 986bp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC system antigen of the invention
XX
SQ Sequence 514 BP; 162 A; 115 C; 96 G; 141 T; 0 U; 0 Other;
QY
Db 2 GGACCTAGAGGCAG 18
430 GGACCTAGAGGCAG 414
RESULT 17
AAS39499/c
ID AAS39499 standard; cDNA; 514 BP.
XX
AC AAS39499;
XX
DT 17-DEC-2001 (first entry)
XX
DE cDNA encoding novel human colon associated polypeptide #152.
XX
KW Human: colon cancer; congenital abnormality; infection; colitis;
KW inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;
KW intestinal inflammatory disorder; malabsorption syndrome; gastric;
KW sigmoid disease; antibacterial; antiviral; antiinflammatory; cytostatic;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200155302-A2.
PD
XX 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001240.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.

QY 2 GGACCTTAGAGCAAG 18
Db 430 GGACCTTAGAGCCAAG 414
RESULT 18
ADBS2225/c
ID ADB32225 standard; cDNA; 514 BP.
XX ADB32225;
AC
XX
XX 04-DEC-2003 (first entry)
DE Human novel colon related polypeptide cDNA SEQ ID NO 162.
XX
XX gene therapy; ss; gene; cancer; liver disorder; hepatitis;
KM neural disorder; Alzheimer's disease; human; colon.
XX
OS Homo sapiens.
PN US2003050231-A1.
XX
PD 13-MAR-2003.
XX
PF 17-JAN-2001; 2001US-00764872.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217486P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.

XX Example 2; SEQ ID NO 7641; 210bp; English.
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX DNA of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 1797 BP; 574 A; 340 C; 360 G; 523 T; 0 U; 0 Other;

XX Query Match 85.6%; Score 15.4; DB 12; Length 1797;
XX Best Local Similarity 94.1%; Pred. No. 5.3e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 502 GGACCTAGAGGCAAG 486

RESULT 21
ADQ18079
ID ADQ18079 standard; DNA; 9645 BP.
AC ADQ18079;
XX 26-AUG-2004 (first entry)
DT 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 896.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
XX Homo sapiens.
XX MO2004048938-A2.
XX 10-JUN-2004.
XX 26-NOV-2003; 2003MO-US038193.
XX 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Aziz N, Ginsburg WM, Zlotnick A;
XX WPI; 2004-441208/41.
XX

PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX Example 2; SEQ ID NO 896; 210bp; English.
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 9645 BP; 2115 A; 2895 C; 2715 G; 1920 T; 0 U; 0 Other;

XX Query Match 85.6%; Score 15.4; DB 12; Length 9645;
XX Best Local Similarity 94.1%; Pred. No. 5.6e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 319 GGACCTAGAGGCAAG 335

RESULT 22
ADZ59509/C
ID ADZ59509 standard; DNA; 20001 BP.
AC ADZ59509;
XX 30-JUN-2005 (first entry)
DT 30-JUN-2005 (first entry)
XX Secondary hyperparathyroidism detection human polymorphic gene, CH13L1.
XX secondary hyperparathyroidism; endocrine-gen.; antihypoid;
XX renal failure; nephrotropic; SNP detection;
XX single nucleotide polymorphism; SNP; gene; ds; CH13L1.
XX Homo sapiens.
XX Key Location/Qualifiers
XX FT 10001
XX variation /tag= a
XX /standard_name= "single nucleotide polymorphism"

XX JP2005102601-A.
XX 21-APR-2005.
XX 30-SEP-2003; 2003JP-00341015.
XX 30-SEP-2003; 2003JP-00341015.
XX (HYUB-) HYUBITTO GENOMICS KK.
XX (JIKI-) UNIV JIKI.
XX WPI; 2005-358641/37.
XX

PT Testing secondary hyperparathyroidism in chronic renal failure patient,
PT involves detecting variation in gene chosen from CACNA1C, CALCR1, CH13L1,
PT EGF, FGFR1, GPR1, GPR56 and GPRK6.
XX Claim 4; SEQ ID NO 3; 138bp; Japanese.
XX

XX The invention relates to a novel method for testing secondary
XX hyperparathyroidism in a chronic renal failure patient. The method
XX involves detecting a variation in a gene chosen from CACNA1C, CALCR1,
XX CH13L1, EGF, FGFR1, GPR1, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNT14,
XX KCNT1, ORCT14, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,
XX IL17R, OSTF1, EGF, MET, TGF1 and VEGF, or detecting the base in a
XX polymorphism region existing in the vicinity of any one of the genes. The
XX invention further comprises a reagent or kit for testing secondary
XX hyperparathyroidism in a chronic renal failure patient. This
XX polynucleotide sequence represents the polymorphism containing human
XX CH13L1 gene of the invention.

XX Sequence 20001 BP; 4773 A; 5041 C; 5158 G; 5029 T; 0 U; 0 Other;

XX Query Match 85.6%; Score 15.4; DB 14; Length 20001;
XX Best Local Similarity 94.1%; Pred. No. 5.8e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGCAAG 18
 |||||
 DB 2601 GGACCTAGAGCAAG 2585

RESULT 23
 ADQ97998/C
 ID ADQ97998 standard; DNA; 22475 BP.
 XX
 AC ADQ97998;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human cancer associated sequence HDL1-038, SEQ ID 975.
 XX
 KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2004060304-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US041389.
 XX
 PR 27-DEC-2002; 2002US-00330773.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR MPI; 2004-543781/52.
 XX

XX New isolated cancer associated nucleic acids comprising at least 10
 PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
 PT cancers such as leukemia and lymphoma.
 XX
 PS Claim 1; SEQ ID NO 975; 199pp; English.
 XX

CC The present invention relates to cancer associated sequences (ADQ97025-
 CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
 CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

XX Sequence 22475 BP; 5898 A; 5414 C; 5434 G; 5709 T; 0 U; 20 Other;
 SQ

Query Match 85.6%; Score 15.4; DB 12; Length 22475;
 Best Local Similarity 94.1%; Pred. No. 5.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGCAAG 18
 |||||
 DB 15390 GGACCTAGAGCAAG 15374

RESULT 24
 ADM69029
 ID ADM69029 standard; DNA; 191150 BP.
 XX
 AC ADM69029;
 XX
 DT 03-JUN-2004 (first entry)
 XX

DE Human platelet derived growth factor receptor alpha wild-type gDNA.
 XX
 KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
 XX wild-type; type III receptor tyrosine kinase; RTK; de; gene.
 XX
 OS Homo sapiens.
 XX

Key	Location/Qualifiers
FT CDS	1..191150
FT	/*tag= b
FT	/product= "Human platelet derived growth factor receptor
FT	alpha wild-type protein"
FT	1..49
FT exon	/*tag= a
FT	/number= 1
FT intron	50..2330
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FT exon	2331..2648
FT	/*tag= d
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FT intron	2649..4902
FT	/*tag= e
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FT exon	4903..5163
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FT	/number= 3
FT intron	5164..6154
FT	/*tag= g
FT	/number= 3
FT exon	6155..6285
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FT	/number= 4
FT intron	6286..8524
FT	/*tag= i
FT	/number= 4
FT exon	8525..8696
FT	/*tag= j
FT	/number= 5
FT intron	8697..8787
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FT exon	8788..8977
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FT intron	8978..166510
FT	/*tag= m
FT	/number= 6
FT exon	166511..166626
FT	/*tag= n
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FT	/*tag= p
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FT exon	170409..170503
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FT	/number= 10
FT exon	170719..170851
FT	/*tag= v
FT	/number= 11
FT intron	170852..173265
FT	/*tag= w
FT	/number= 11
FT exon	173266..173370
FT	/*tag= x

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FT      /number= 12
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FT      174394..176193
FT      /*tag= ac
FT      /number= 14
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FT      /number= 15
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FT      /*tag= af
FT      /number= 16
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FT      /number= 21
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FT      /number= 22
FT      WO2003105773-A2.
FT      PN
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FT      PD
FT      24-DEC-2003.
FT      XX
FT      PF
FT      13-JUN-2003; 2003WO-US018901.
FT      XX
FT      PR
FT      13-JUN-2002; 2002US-0389107P.
FT      XX
FT      PR
FT      08-JAN-2003; 2003US-0438899P.
FT      XX
FT      PA
FT      (UYOR-) UNIV OREGON HEALTH SCI.
FT      (DAND) DANA FARBER CANCER INST. INC.

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PA      (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA      (USGO) US DEPT. VETERANS AFFAIRS.
XX
XX      PI
XX      Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX      WPI; 2004-082052/08.
XX      DR
XX      P-PSDB; ADM69012.
XX
XX      PT
XX      New isolated variant platelet derived growth factor alpha (PDGFRA)
XX      polypeptide, useful for screening for a compound useful in influencing
XX      PDGFRA-mediated neoplasia in a mammal.
XX
XX      PS
XX      Example 1; SEQ ID NO 19; 302pp; English.
XX
XX      CC
XX      The invention relates to a novel isolated variant platelet derived growth
XX      factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
XX      invention is a type III receptor tyrosine kinase (RTK) and may be useful
XX      for screening for a compound that may influence PDGFRA-mediated neoplasia
XX      in a mammal. The current sequence is that of the human PDGFRA wild-type
XX      genomic DNA of the invention.
XX
XX      SQ
XX      Sequence 191150 BP; 55223 A; 39036 C; 39352 G; 56412 T; 0 U; 1127 Other;
XX
XX      Query Match
XX      85.6%; Score 15.4; DB 12; Length 191150;
XX      Best Local Similarity 94.1%; Pred. No. 6.2e+02;
XX      Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      Qy
XX      2 GGACCCCTAGAGGCAAG 18
XX      117726 GGACCCCTAGAGGCAAG 117742
XX
XX      Db
XX
XX      RESULT 25
XX      ABZ07598
XX      ID ABZ07598 standard; DNA; 50 BP.
XX
XX      AC
XX      ABZ07598;
XX
XX      DT
XX      09-JAN-2003 (first entry)
XX
XX      DE
XX      Human leukocyte gene expression profiling probe SEQ ID NO 7589.
XX
XX      KW
XX      T7; leukocyte; gene expression profiling; allograft rejection;
XX      atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX      rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX      ss.
XX
XX      OS
XX      Homo sapiens.
XX
XX      PN
XX      WO200257414-A2.
XX
XX      PD
XX      25-JUL-2002.
XX
XX      PF
XX      22-OCT-2001; 2001WO-US047856.
XX
XX      PR
XX      20-OCT-2000; 2000US-0241994P.
XX      PR
XX      08-JUN-2001; 2001US-0296764P.
XX
XX      PA
XX      (BIOC-) BIOCARDIA INC.
XX
XX      PI
XX      Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX      Ly N, Woodward R, Quertermous T, Johnson F;
XX      WPI; 2002-636525/68.
XX
XX      DR
XX
XX      PT
XX      New system for leukocyte expression profiling, diagnosing a disease, or
XX      monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX      or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX      PS
XX      Claim 1; Page 572; ODP; English.
XX
XX      CC
XX      The invention relates to a system for detecting gene expression, which
XX      comprises one or two isolated DNA molecules that detect expression of a

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CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX

XX Sequence 50 BP; 12 A; 15 C; 11 G; 12 T; 0 U; 0 Other;
SQ

Query Match 83.3%; Score 15; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAA 16
DB 18 GGACCTTAGAGGCAA 32

RESULT 26
ADP10220
ID ADP10220 standard; DNA; 50 BP.
XX
XX ADP10220;
AC
XX 12-AUG-2004 (first entry)
DT
XX
XX 50-mer oligonucleotide marker probe of the invention #229.
DE
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004042346-A2.
PN
XX
XX 21-MAY-2004.
PD
XX
XX 24-APR-2003; 2003WO-US012946.
PF
XX
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
PI
XX MPI: 2004-400724/37.
DR
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
PT
XX
XX Claim 2; SEQ ID NO 229; 1762bp; English.
PS

The present invention relates to diagnosing or monitoring transplant
rejection, e.g. cardiac or kidney transplant rejection, in an individual
comprises detecting the expression level of one or more genes. The
methods, system and kits are useful in diagnosing or monitoring
transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
islet, lung, bone marrow or stem cell, transplant rejection,
xenotransplant rejection or mechanical organ replacement rejection, in an
individual. The method is also useful in assessing the immune status of
an individual. The methods are also useful in diagnosing and monitoring
diseases that involve the immune system, e.g. rheumatoid arthritis,
lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
viral, bacterial or fungal infection. The present sequence represents a
50 mer oligonucleotide marker for diagnosis and monitoring of allograft

CC rejection and other disorders.
XX
XX Sequence 50 BP; 12 A; 15 C; 11 G; 12 T; 0 U; 0 Other;
SQ

Query Match 83.3%; Score 15; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAA 16
DB 18 GGACCTTAGAGGCAA 32

RESULT 27
AAI76987/C
ID AAI76987 standard; DNA; 51 BP.
XX
XX AAI76987;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:3928.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; db.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX
XX 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shinkets RA, Leach M;
PI
XX MPI: 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PT
XX
XX Claim 1; Page 1254; 2653bp; English.
PS

AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (II) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX

XX Sequence 51 BP; 9 A; 12 C; 19 G; 11 T; 0 U; 0 Other;
SQ

Query Match 83.3%; Score 15; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAA 16
 Db 17 GGACCTTAGAGGCAA 3

RESULT 28

AA176986/c

ID AA176986 standard; DNA; 51 BP.

XX AA176986;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3927.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KM protein therapy; vaccine; probe; diagnostic assay; detection;
 KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX MO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
 therapy.

XX Claim 1; Page 1253; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

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CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

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CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
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CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
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CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
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CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

RESULT 29

AB095689

ID AB095689 standard; DNA; 75 BP.

XX AB095689;

DT 28-OCT-2002 (first entry)

DE Tumour suppression-related oligonucleotide #1340.

XX Tumour; cytostatic; antiviral; neuroprotective; nocotropic; neuroleptic;

XX Tumour suppression; tumour reversion; apoptosis; viral resistance; human;

XX Viral infection; cell degeneration disease; neurodegeneration; ds;

XX Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.

XX Homo sapiens.

XX FR2819824-A1.

XX 26-JUL-2002.

XX 23-JAN-2001; 2001FR-00000899.

XX 23-JAN-2001; 2001FR-00000899.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Telerman A, Amson R, Tuijnder M, Susini L;

XX WPI; 2002-610803/66.

PT New nucleic acid implicated e.g. in tumor suppression, useful for
 PT diagnosis of tumors, viral infection and cellular degeneration and for
 PT drug screening.

XX Claim 1; Page 375; 623pp; French.

CC The present invention relates to novel human nucleic acid sequences (I).

CC The present invention relates to novel human nucleic acid sequences (I).

CC The present invention relates to novel human nucleic acid sequences (I).

CC The present invention relates to novel human nucleic acid sequences (I).

CC The present invention relates to novel human nucleic acid sequences (I).

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CC The present invention relates to novel human nucleic acid sequences (I).

CC The present invention relates to novel human nucleic acid sequences (I).

CC The present invention relates to novel human nucleic acid sequences (I).

XX Human secreted protein 5' EST, SEQ ID NO: 28900.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic; forensic; gene therapy and chromosome mapping procedures.

PS Claim 1; SEQ ID NO 28900; 71bp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors

CC Sequence 163 BP; 35 A; 57 C; 41 G; 30 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 3; Length 163;

Best Local Similarity 100.0%; Pred No. 7.9e+02; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0;

OY 2 GGACCTTAGAGCAA 16
 |||||
 DB 148 GGACCTTAGAGCAA 162

Search completed: April 15, 2006, 20:26:40
 Job time : 692 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 18:12:40 ; Search time 418 Seconds

(without alignments)
173.447 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15.4	85.6	539	9	US-10-301-480-668554
3	15.4	85.6	574	6	US-09-925-065A-504327
4	15.4	85.6	738	6	US-09-925-065A-65294
5	15.4	85.6	738	6	US-09-925-065A-65295
6	15.4	85.6	738	6	US-09-925-065A-65296
7	15.4	85.6	738	6	US-09-925-065A-65297
8	15.4	85.6	738	6	US-10-301-480-16653
9	15.4	85.6	738	9	US-10-301-480-16654
10	15.4	85.6	738	10	US-10-301-480-16655
11	15.4	85.6	738	10	US-10-301-480-779942
12	15.4	85.6	738	10	US-10-301-480-779943
13	15.4	85.6	738	10	US-10-301-480-779944
14	15.4	85.6	738	10	US-10-301-480-779945
15	15.4	85.6	738	10	US-10-301-480-779946
16	15.4	85.6	738	10	US-10-301-480-779947
17	15.4	85.6	738	10	US-10-301-480-779948
18	15.4	85.6	738	10	US-10-301-480-779949

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21	15.4	85.6	22475	14	US-10-330-773-975	Sequence 975, App
22	15.4	85.6	100000	14	US-11-124-367A-5024	Sequence 5024, App
23	15.4	85.6	171732	14	US-11-121-086-98	Sequence 98, App
24	15.4	85.6	171732	14	US-11-101-244-1292346	Sequence 1292346, App
25	15.4	85.6	171732	14	US-11-101-244-1292367	Sequence 1292367, App
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C 92	14.4	80.0	584	10	US-10-301-480-682498	Sequence 682498,	165	14	77.8	608	6	US-09-925-065A-862400	Sequence 862400,
C 93	14.4	80.0	588	6	US-09-925-065A-423040	Sequence 423040,	166	14	77.8	613	6	US-09-925-065A-873046	Sequence 873046,
C 94	14.4	80.0	589	6	US-09-925-065A-73423	Sequence 73423, A	167	14	77.8	613	6	US-09-925-065A-873047	Sequence 873047,
C 95	14.4	80.0	589	6	US-09-925-065A-73424	Sequence 73424, A	168	14	77.8	623	6	US-09-925-065A-867206	Sequence 867206,
C 96	14.4	80.0	589	6	US-09-925-065A-73425	Sequence 73425, A	169	14	77.8	623	6	US-09-925-065A-867207	Sequence 867207,
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C 98	14.4	80.0	589	9	US-10-301-480-174663	Sequence 174663,	171	14	77.8	640	6	US-09-925-065A-678312	Sequence 678312,
C 99	14.4	80.0	589	9	US-10-301-480-174664	Sequence 174664,	172	14	77.8	640	6	US-09-925-065A-678313	Sequence 678313,
C 100	14.4	80.0	589	10	US-10-301-480-1786071	Sequence 1786071,	173	14	77.8	680	6	US-09-925-065A-709785	Sequence 709785,
C 101	14.4	80.0	589	10	US-10-301-480-788072	Sequence 788072,	174	14	77.8	777	10	US-10-301-480-1528233	Sequence 1528233,
C 102	14.4	80.0	589	10	US-10-301-480-788073	Sequence 788073,	175	14	77.8	777	10	US-10-301-480-1528242	Sequence 1528242,
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C 104	14.4	80.0	593	6	US-09-925-065A-109777	Sequence 109777,	177	14	77.8	1404	9	US-10-932-182A-79871	Sequence 79871, A
C 105	14.4	80.0	594	6	US-09-925-065A-819764	Sequence 819764,	178	14	77.8	1588	8	US-10-750-185-25515	Sequence 25515, A
C 106	14.4	80.0	594	6	US-09-925-065A-819765	Sequence 819765,	179	14	77.8	1588	8	US-10-750-185-25515	Sequence 25515, A
C 107	14.4	80.0	599	6	US-10-301-480-21094	Sequence 21094, A	180	14	77.8	2025	6	US-09-925-065A-94759	Sequence 94759, A
C 108	14.4	80.0	599	10	US-10-301-480-634503	Sequence 634503,	181	14	77.8	2025	6	US-09-925-065A-94760	Sequence 94760, A
C 109	14.4	80.0	600	10	US-10-301-480-518947	Sequence 518947,	182	14	77.8	2025	6	US-09-925-065A-196001	Sequence 196001, A
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C 114	14.4	80.0	601	10	US-10-301-480-946707	Sequence 946707,	187	14	77.8	2025	10	US-10-301-480-809411	Sequence 809411,
C 115	14.4	80.0	606	6	US-09-925-065A-431300	Sequence 431300,	188	14	77.8	2025	10	US-10-301-480-809412	Sequence 809412,
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C 117	14.4	80.0	610	6	US-09-925-065A-462218	Sequence 462218,	190	14	77.8	241805	8	US-10-925-561-13215	Sequence 13215, A
C 118	14.4	80.0	610	6	US-09-925-065A-462218	Sequence 462218,	191	14	77.8	341511	9	US-10-925-561-13215	Sequence 13215, A
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C 141	14.4	80.0	2746	8	US-10-750-185-46191	Sequence 46191, A	214	13.8	76.7	201	14	US-11-124-367A-15107	Sequence 15107, A
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C 147	14.4	80.0	98560	4	US-10-995-561-13323	Sequence 13323, A	220	13.8	76.7	445	10	US-10-301-480-497970	Sequence 497970,
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285 13.8 76.7 563 6 US-09-925-065A-174686 Sequence 174686,
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ALIGNMENTS

RESULT 1
US-10-301-480-55145
; Sequence 55145, Application US/10301480
; Publication No. US2006057564A1
; GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55145
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-55145

Query Match 85.6%; Score 15.4; DB 9; Length 539;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGACCTGAGGCAAG 18
Db 63 GGACCTGAGGCAAG 79

RESULT 2
US-10-301-480-668554
; Sequence 668554, Application US/10301480
; Publication No. US2006057564A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 668554
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-668554

Query Match 85.6%; Score 15.4; DB 10; Length 539;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGACCTGAGGCAAG 18
Db 63 GGACCTGAGGCAAG 79

RESULT 3
US-09-925-065A-504327/c
; Sequence 504327, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147


```
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 504327
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-504327
```

```
Query Match      85.6%; Score 15.4; DB 6; Length 574;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
         |||||
Db      361 GGACCCCAAGGCAAG 345
```

```
RESULT 4
US-09-925-065A-65294/c
; Sequence 65294, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65294
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65294
```

```
Query Match      85.6%; Score 15.4; DB 6; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
         |||||
Db      498 GGACCTTAGAGGCAAG 482
```

```
RESULT 5
US-09-925-065A-65295/c
; Sequence 65295, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
```

```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65295
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65295
```

```
Query Match      85.6%; Score 15.4; DB 6; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
         |||||
Db      498 GGACCTTAGAGGCAAG 482
```

```
RESULT 6
US-09-925-065A-65296/c
; Sequence 65296, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65296
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-65296
```

```
Query Match      85.6%; Score 15.4; DB 6; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GGACCTTAGAGGCAAG 18
         |||||
Db      498 GGACCTTAGAGGCAAG 482
```

```
RESULT 7
US-10-301-480-165533/c
; Sequence 16533, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
```

FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 166533
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166533

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
Db 498 GGACCTAGAGGCAAG 482

RESULT 8
US-10-301-480-166534/c
Sequence 166534, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 166534
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166534

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
Db 498 GGACCTAGAGGCAAG 482

RESULT 9
US-10-301-480-166535/c
Sequence 166535, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 166535
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166535

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
Db 498 GGACCTAGAGGCAAG 482

RESULT 10
US-10-301-480-779942/c
Sequence 779942, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 779942
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-779942

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
Db 498 GGACCTAGAGGCAAG 482

RESULT 11
US-10-301-480-779943/c
Sequence 779943, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 779943
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-779943

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 498 GGACCTAGAGCAAG 482

RESULT 12
US-10-301-480-779944/c
; Sequence 779944, Application US/10301480
; Publication No. US2006005754A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779944
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-779944

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 498 GGACCTAGAGCAAG 482

RESULT 13
US-10-750-185-61166
; Sequence 61166, Application US/10750185
; Publication No. US20050280603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61166
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Bovine 19866881037774
US-10-750-185-61166

Query Match 85.6%; Score 15.4; DB 8; Length 1155;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 869 GGACCTAGAGCAAG 885

RESULT 14
US-10-750-623-61166
; Sequence 61166, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61166
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Bovine 19866881037774
US-10-750-623-61166

Query Match 85.6%; Score 15.4; DB 8; Length 1155;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
|||
DB 869 GGACCTAGAGCAAG 885

RESULT 15
US-10-932-182A-2596/c
; Sequence 2596, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2596
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2596

Query Match 85.6%; Score 15.4; DB 9; Length 1206;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGACCTAGAGCAAA 17
|||
DB 1141 CGACCTAGAGCAAA 1125

RESULT 16
US-10-932-182A-2596/c
; Sequence 2596, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA

```

; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 2596
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-2596

Query Match      85.6%; Score 15.4; DB 9; Length 1206;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGACCTTAGGCGCAA 17
Db      1141 CGGACCTTAGAGACAAA 1125

RESULT 17
US-11-096-568A-33576/c
; Sequence 33576, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PU52
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO: 33576
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(1806)
; OTHER INFORMATION: Ceres Seq. ID no. 13603467
; US-11-096-568A-33576

Query Match      85.6%; Score 15.4; DB 11; Length 1806;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGACCTTAGAGGCAAG 18
Db      915 GGACCTTAGAGGCAATG 899

RESULT 18
US-11-096-568A-2408/c
; Sequence 2408, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PU52
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO: 2408
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
```

```

; LOCATION: (1)-(1862)
; OTHER INFORMATION: Ceres Seq. ID no. 14312112
; US-11-096-568A-2408

Query Match      85.6%; Score 15.4; DB 11; Length 1862;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGACCTTAGAGGCAAG 18
Db      948 GGACCTTAGAGGCAATG 932

RESULT 19
US-11-128-061-856/c
; Sequence 856, Application US/11128061
; Publication No. US2006003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997,027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 856
; LENGTH: 8703
; TYPE: DNA
; ORGANISM: Mesocricetus auratus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (279)-(8703)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (293)-(321)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (331)-(349)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (402)-(414)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (417)-(446)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1384)-(1455)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1728)-(1776)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2778)-(2795)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (3235)..(3257)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3287)..(3340)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3342)..(3362)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4001)..(4025)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4437)..(4454)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4895)..(4922)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7677)..(7701)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7861)..(7903)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7932)..(7949)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (8381)..(8418)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-856

Query Match 85.6%; Score 15.4; DB 14; Length 8703;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
DB 6031 GGACCTAGAGCAAG 6015

RESULT 20
US-11-128-049-856/c
Sequence 856, Application US/11128049
Publication No. US20060010513A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 856
LENGTH: 8703

TYPE: DNA
ORGANISM: Mesocricetus auratus
FEATURE:
NAME/KEY: misc feature
LOCATION: (279)..(291)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (293)..(321)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (331)..(349)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (402)..(414)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (417)..(446)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1384)..(1455)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1728)..(1776)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (2778)..(2795)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3235)..(3257)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3287)..(3340)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (3342)..(3362)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4001)..(4025)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4437)..(4454)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (4895)..(4922)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7677)..(7701)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7861)..(7903)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (7932)..(7949)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (8381)..(8418)

OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-856

Query Match 85.6%; Score 15.4; DB 14; Length 8703;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
DB 6031 GGACCTTAGAGGCAAG 6015

RESULT 21

US-10-330-773-975/c
Sequence 975, Application US/10330773
Publication No. US20060040262a1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 52945201300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 975
LENGTH: 22475
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)..(22475)
OTHER INFORMATION: n = A,T,C or G
US-10-330-773-975

Query Match 85.6%; Score 15.4; DB 9; Length 22475;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
DB 15390 GGACCTTAGAGGCAAG 15374

RESULT 22

US-11-124-367A-5024
Sequence 5024, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CU001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5024
LENGTH: 100000
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-5024

Query Match 85.6%; Score 15.4; DB 14; Length 100000;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
DB 27957 GGACCTTAGAGGCAAG 27973

RESULT 23

US-11-121-086-98/c
Sequence 98, Application US/1121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 98
LENGTH: 171732
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-98

Query Match 85.6%; Score 15.4; DB 14; Length 171732;
Best Local Similarity 94.1%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
DB 12979 GGACCTTAGAGGCAAG 12963

RESULT 24

US-11-101-244-1292346
Sequence 1292346, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Pharmacia, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1292346
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1292346

Query Match 83.3%; Score 15; DB 12; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCA 16
DB 4 GGACCTTAGAGGCA 18

RESULT 25

```
US-11-101-244-1292367
; Sequence 1292367, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1292367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1292367
```

```
Query Match      83.3%; Score 15; DB 12; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      2 GGACCTAGAGGCAA 16
DB      1 GGACCTUAGAGGCAA 15
```

```
RESULT 26
US-11-083-784-1292346
; Sequence 1292346, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1292346
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1292346
```

```
Query Match      83.3%; Score 15; DB 13; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGGCAA 16
DB      4 GGACCTUAGAGGCAA 18
```

```
RESULT 27
US-11-083-784-1292367
; Sequence 1292367, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1292367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1292367
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Query Match      83.3%; Score 15; DB 13; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGGCAA 16
DB      1 GGACCTUAGAGGCAA 15
```

```
RESULT 28
US-10-310-914A-965984/c
; Sequence 965984, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Yvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 965984
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-965984
```

```
Query Match      83.3%; Score 15; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGGCAA 16
DB      17 GGACCTAGAGGCAA 3
```

```
RESULT 29
US-09-925-065A-799050/c
; Sequence 799050, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 799050
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-799050
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Query Match      83.3%; Score 15; DB 6; Length 640;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGCAA 16
      |||||
Db      580 GGACCTAGAGCAA 566
```

```
RESULT 30
US-09-925-065A-799051/C
; Sequence 799051, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 799051
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-799051
```

```
Query Match      83.3%; Score 15; DB 6; Length 640;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGCAA 16
      |||||
Db      580 GGACCTAGAGCAA 566
```

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Search completed: April 15, 2006, 18:19:53
Job time : 425 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 18:09:33 ; Search time 806 Seconds
(without alignments)
184.676 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggaccctagagcaag 18

Scoring table: IDENTITY_NUC

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-727-358-5	Sequence 5, Appl1
2	18	100.0	18	US-10-727-358-15	Sequence 15, Appl1
3	18	100.0	18	US-10-727-358-28	Sequence 28, Appl1
4	18	100.0	25	US-11-036-317-881396	Sequence 881396, Appl1
5	18	100.0	25	US-11-036-317-904638	Sequence 904638, Appl1
6	18	100.0	25	US-11-036-317-910916	Sequence 910916, Appl1
7	18	100.0	120	US-10-727-358-1	Sequence 1, Appl1
8	18	100.0	121	US-10-727-358-25	Sequence 25, Appl1
9	18	100.0	2601	US-10-727-358-24	Sequence 24, Appl1
10	18	100.0	2632	US-10-085-117-33	Sequence 33, Appl1
11	18	100.0	4034	US-10-085-117-32	Sequence 32, Appl1
12	18	100.0	4094	US-10-727-358-11	Sequence 11, Appl1
13	16.4	91.1	25	US-11-036-317-881395	Sequence 881395, Appl1
14	16.4	91.1	25	US-11-036-317-904637	Sequence 904637, Appl1
15	16.4	91.1	25	US-11-036-317-910915	Sequence 910915, Appl1
16	16	88.9	16	US-10-727-358-8	Sequence 8, Appl1
17	16	88.9	25	US-11-036-317-928166	Sequence 928166, Appl1
18	15.4	85.6	233	US-10-242-535A-12378	Sequence 12378, A
19	15.4	85.6	233	US-10-085-783A-12378	Sequence 12378, A
20	15.4	85.6	376	US-09-964-824A-522	Sequence 522, Appl1
21	15.4	85.6	376	US-09-969-708-67	Sequence 67, Appl1
22	15.4	85.6	376	US-10-843-61A-5825	Sequence 5825, Appl1
23	15.4	85.6	376	US-10-843-61A-7538	Sequence 7538, Appl1

24	15.4	85.6	283	US-10-425-115-110504	Sequence 110504, Appl1
25	15.4	85.6	481	US-10-027-632-141547	Sequence 141547, Appl1
26	15.4	85.6	481	US-10-027-632-141547	Sequence 141547, Appl1
27	15.4	85.6	514	US-09-764-872-162	Sequence 162, Appl1
28	15.4	85.6	546	US-10-027-632-202268	Sequence 202268, Appl1
29	15.4	85.6	546	US-10-027-632-202268	Sequence 202268, Appl1
30	15.4	85.6	547	US-10-424-599-52757	Sequence 52757, A
31	15.4	85.6	574	US-09-925-065A-504327	Sequence 504327, A
32	15.4	85.6	611	US-10-027-632-228051	Sequence 228051, A
33	15.4	85.6	611	US-10-027-632-228051	Sequence 228051, A
34	15.4	85.6	738	US-09-925-065A-65294	Sequence 65294, A
35	15.4	85.6	738	US-09-925-065A-65295	Sequence 65295, A
36	15.4	85.6	738	US-09-925-065A-65296	Sequence 65296, A
37	15.4	85.6	751	US-10-027-632-19033	Sequence 19033, A
38	15.4	85.6	751	US-10-027-632-19033	Sequence 19033, A
39	15.4	85.6	1797	US-10-723-860-7641	Sequence 7641, Appl1
40	15.4	85.6	9645	US-10-723-860-896	Sequence 896, Appl1
41	15.4	85.6	9645	US-10-756-149-895	Sequence 895, Appl1
42	15.4	85.6	314364	US-10-917-647-3	Sequence 3, Appl1
43	15	83.3	50	US-10-131-827-7589	Sequence 7589, Appl1
44	15	83.3	75	US-10-466-894-1339	Sequence 1339, Appl1
45	15	83.3	265	US-10-242-535A-13707	Sequence 13707, A
46	15	83.3	265	US-10-085-783A-13707	Sequence 13707, A
47	15	83.3	285	US-10-424-599-34328	Sequence 34328, A
48	15	83.3	320	US-10-242-535A-6362	Sequence 6362, Appl1
49	15	83.3	320	US-10-085-783A-6362	Sequence 6362, Appl1
50	15	83.3	327	US-10-242-535A-13737	Sequence 13737, A
51	15	83.3	327	US-10-085-783A-13737	Sequence 13737, A
52	15	83.3	327	US-10-085-783A-13737	Sequence 13737, A
53	15	83.3	342	US-09-878-178-1996	Sequence 1996, Appl1
54	15	83.3	342	US-10-046-935-1996	Sequence 1996, Appl1
55	15	83.3	342	US-10-146-502-1996	Sequence 1996, Appl1
56	15	83.3	412	US-09-918-995-37155	Sequence 37155, A
57	15	83.3	444	US-09-822-846-548	Sequence 548, Appl1
58	15	83.3	478	US-09-918-995-16549	Sequence 16549, A
59	15	83.3	554	US-09-764-869-334	Sequence 334, Appl1
60	15	83.3	554	US-10-091-504-334	Sequence 334, Appl1
61	15	83.3	554	US-10-227-577-334	Sequence 334, Appl1
62	15	83.3	576	US-10-027-632-282238	Sequence 282238, Appl1
63	15	83.3	576	US-10-027-632-282238	Sequence 282238, Appl1
64	15	83.3	600	US-10-956-157-7765	Sequence 7765, Appl1
65	15	83.3	606	US-10-027-632-309560	Sequence 309560, A
66	15	83.3	606	US-10-027-632-309560	Sequence 309560, A
67	15	83.3	606	US-10-027-632-309560	Sequence 309560, A
68	15	83.3	606	US-10-027-632-309560	Sequence 309560, A
69	15	83.3	627	US-09-971-392-213	Sequence 213, Appl1
70	15	83.3	640	US-09-925-065A-799050	Sequence 799050, A
71	15	83.3	640	US-09-925-065A-799051	Sequence 799051, A
72	15	83.3	640	US-09-925-065A-799052	Sequence 799052, A
73	15	83.3	669	US-09-925-065A-799053	Sequence 799053, A
74	15	83.3	669	US-09-925-065A-799053	Sequence 799053, A
75	15	83.3	764	US-10-956-157-2530	Sequence 2530, Appl1
76	15	83.3	779	US-09-822-846-549	Sequence 549, Appl1
77	15	83.3	782	US-09-890-688-95	Sequence 95, Appl1
78	15	83.3	2278	US-10-108-260A-62	Sequence 62, Appl1
79	15	83.3	2399	US-10-641-643-508	Sequence 508, Appl1
80	15	83.3	5760	US-11-097-143-33785	Sequence 33785, A
81	15	83.3	44449	US-10-087-129-280	Sequence 280, Appl1
82	15	83.3	122937	US-10-322-281-694	Sequence 694, Appl1
83	15	83.3	42109	US-10-367-094-132	Sequence 132, Appl1
84	14.8	82.2	399	US-10-915-740A-638	Sequence 638, Appl1
85	14.8	82.2	486	US-10-425-115-129192	Sequence 129192, A
86	14.8	82.2	529	US-10-925-065A-758596	Sequence 758596, A
87	14.8	82.2	566	US-09-925-065A-758596	Sequence 758596, A
88	14.8	82.2	568	US-10-437-963-25209	Sequence 25209, A
89	14.8	82.2	588	US-09-925-065A-585830	Sequence 585830, A
90	14.8	82.2	588	US-09-925-065A-585831	Sequence 585831, A
91	14.8	82.2	588	US-09-925-065A-585832	Sequence 585832, A
92	14.8	82.2	588	US-09-925-065A-585833	Sequence 585833, A
93	14.8	82.2	594	US-09-925-065A-126082	Sequence 126082, A
94	14.8	82.2	624	US-09-925-065A-894131	Sequence 894131, A
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ALIGNMENTS

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RESULT 1
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; Sequence 5, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: King, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS

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; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGGACCTTAGAGCAAG 18

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; Sequence 15, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: King, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sense oligonucleotide
US-10-727-358-15
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; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: King, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED

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;; TITLE OF INVENTION: TUMORIGENESIS
;; FILE REFERENCE: 1216-1-006CIP
;; CURRENT APPLICATION NUMBER: US/10/727,358
;; CURRENT FILING DATE: 2003-12-03
;; PRIOR APPLICATION NUMBER: 60/384,228
;; PRIOR FILING DATE: 2002-05-30
;; PRIOR APPLICATION NUMBER: 60/460,023
;; PRIOR FILING DATE: 2003-04-03
;; PRIOR APPLICATION NUMBER: PCT/US03/16961
;; PRIOR FILING DATE: 2003-05-29
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;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: antisense oligonucleotide
US-10-727-358-28

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RESULT 4
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; Sequence 881396, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
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US-11-036-317-881396

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RESULT 5
US-11-036-317-904638
; Sequence 904638, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174

;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 904638
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-904638

Query Match 100.0%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGAGGCAAG 18
Db 2 CGGACCTTAGAGGCAAG 19

RESULT 6
US-11-036-317-910916
; Sequence 910916, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 910916
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-910916

Query Match 100.0%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTTAGAGGCAAG 18
Db 1 CGGACCTTAGAGGCAAG 18

RESULT 7
US-10-727-358-1
; Sequence 1, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDiate
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-358-1

Query Match 100.0%; Score 18; DB 8; Length 120;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTAGAGGCAAG 18
|||
DB 91 CGGACCTAGAGGCAAG 108

RESULT 8
US-10-727-358-25
; Sequence 25, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-358-25

Query Match 100.0%; Score 18; DB 8; Length 121;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
|||
DB 91 CGGACCTAGAGGCAAG 108

RESULT 9
US-10-727-358-24
; Sequence 24, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-358-24

Query Match 100.0%; Score 18; DB 8; Length 2601;

Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTAGAGGCAAG 18
|||
DB 187 CGGACCTAGAGGCAAG 204

RESULT 10
US-10-085-117-33
; Sequence 33, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-085-117-33

Query Match 100.0%; Score 18; DB 6; Length 2622;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
|||
DB 214 CGGACCTAGAGGCAAG 231

RESULT 11
US-10-085-117-32
; Sequence 32, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4094
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-085-117-32

Query Match 100.0%; Score 18; DB 6; Length 4094;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
|||
DB 296 CGGACCTAGAGGCAAG 313

RESULT 12
US-10-727-358-11
; Sequence 11, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:

APPLICANT: Memorial Sloan-Kettering Cancer Center
APPLICANT: Kolesnick, Richard N.
APPLICANT: Xing, Hong-Mei R.
TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
TITLE OF INVENTION: TUMORIGENESIS
FILE REFERENCE: 1216-1-006CIP
CURRENT APPLICATION NUMBER: US/10/727,358
CURRENT FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: 60/384,228
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/460,023
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: PCT/US03/16961
PRIOR FILING DATE: 2003-05-29
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 4094
TYPE: DNA
ORGANISM: Mus musculus
US-10-727-358-11

Query Match 100.0%; Score 18; DB 8; Length 4094;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 296 CGGACCTAGAGGCAAG 313

RESULT 13
US-11-036-317-881395
Sequence 881395, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 881395
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-881395

Query Match 91.1%; Score 16.4; DB 10; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 4 CGGACCTAGAGGCAAG 21

RESULT 14
US-11-036-317-904637
Sequence 904637, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 904637
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-904637

Query Match 91.1%; Score 16.4; DB 10; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 2 CGGACCTAGAGGCAAG 19

RESULT 15
US-11-036-317-910915
Sequence 910915, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 910915
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-910915

Query Match 91.1%; Score 16.4; DB 10; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
DB 1 CGGACCTAGAGGCAAG 18

RESULT 16
US-10-727-358-8/c
Sequence 8, Application US/10727358
Publication No. US20050037455A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
APPLICANT: Kolesnick, Richard N.
APPLICANT: Xing, Hong-Mei R.
TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATE
TITLE OF INVENTION: TUMORIGENESIS
FILE REFERENCE: 1216-1-006CIP
CURRENT APPLICATION NUMBER: US/10/727,358
CURRENT FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: 60/384,228
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/460,023
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: PCT/US03/16961
PRIOR FILING DATE: 2003-05-29
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence

```
FEATURE:
OTHER INFORMATION: antisense oligonucleotide
US-10-727-358-8

Query Match      88.9%; Score 16; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACCTAGAGGCAAG 18
      |||||
Db      16 GACCTAGAGGCAAG 1

RESULT 17
US-11-036-317-928166
Sequence 928166, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 928166
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-928166

Query Match      88.9%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GACCTAGAGGCAAG 18
      |||||
Db      1 GACCTAGAGGCAAG 16

RESULT 18
US-10-242-535A-12378/c
Sequence 12378, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12378
LENGTH: 233
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (13)-(13)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
```

```
NAME/KEY: misc_feature
LOCATION: (28)-(28)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (34)-(34)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)-(39)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)-(66)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-12378

Query Match      85.6%; Score 15.4; DB 7; Length 233;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGACCTAGAGGCAAG 18
      |||||
Db      188 GGACCTAGAGGCAAG 172

RESULT 19
US-10-085-783A-12378/c
Sequence 12378, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12378
LENGTH: 233
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (13)-(13)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28)-(28)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (34)-(34)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)-(39)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66)-(66)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-12378

Query Match      85.6%; Score 15.4; DB 7; Length 233;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
```

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
Db 188 GGACCTAGAGGCAAG 172

RESULT 20
US-09-964-824A-522/c
; Sequence 522, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-522

Query Match 85.6%; Score 15.4; DB 3; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGAGGCAAG 18
Db 107 GGACCTAGAGGCAAG 91

RESULT 21
US-09-969-708-67/c
; Sequence 67, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-67

Query Match 85.6%; Score 15.4; DB 3; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGAGGCAAG 18
Db 107 GGACCTAGAGGCAAG 91

RESULT 22
US-10-843-641A-5825/c
; Sequence 5825, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5825
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5825

Query Match 85.6%; Score 15.4; DB 9; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGAGGCAAG 18
Db 107 GGACCTAGAGGCAAG 91

RESULT 23
US-10-843-641A-7538/c
; Sequence 7538, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824

PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: Patent version 3.0
SEQ ID NO 7538
LENGTH: 376
TYPE: DNA
ORGANISM: Homo sapiens
US-10-843-641A-7538

Query Match 85.6%; Score 15.4; DB 9; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 107 GGACCTAGAGGCAAG 91

RESULT 24

US-10-425-115-110504
Sequence 110504, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 110504
LENGTH: 383
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: MFT4577_32272C.1
US-10-425-115-110504

Query Match 85.6%; Score 15.4; DB 8; Length 383;
Best Local Similarity 94.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 3 GGACCTAGAGGCAAG 19

RESULT 25

US-10-027-632-141547
Sequence 141547, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 141547
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-10-027-632-141547

Query Match 85.6%; Score 15.4; DB 5; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 255 GGACCTAGAGGCAAG 271

RESULT 26

US-10-027-632-141547
Sequence 141547, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 141547
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-10-027-632-141547

Query Match 85.6%; Score 15.4; DB 6; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGCAAG 18
DB 255 GGACCTAGAGGCAAG 271

RESULT 27

US-09-764-872-162/C
Sequence 162, Application US/09764872

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; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-162
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Query Match      85.6%; Score 15.4; DB 3; Length 514;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGGCAAG 18
      |||||
DB      430 GGACCTAGAGGCCAAG 414
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RESULT 28

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US-10-027-632-202268
; Sequence 202268, Application US/10027632
; Publication No. US2002019871A1
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202268
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202268
```

```
Query Match      85.6%; Score 15.4; DB 5; Length 546;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGGCAAG 18
      |||||
DB      62 GGACCTAGAGGCAAG 78
```

RESULT 29

```
US-10-027-632-202268
; Sequence 202268, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202268
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202268
```

```
Query Match      85.6%; Score 15.4; DB 6; Length 546;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 GGACCTAGAGGCAAG 18
      |||||
DB      62 GGACCTAGAGGCAAG 78
```

RESULT 30

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US-10-424-599-52757
; Sequence 52757, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 52757
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18652C.1
US-10-424-599-52757
```

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Query Match      85.6%; Score 15.4; DB 7; Length 547;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY      2 GGACCTAGAGGCAAG 18
      |||||
DB      366 GGACCTAGAGGCAAG 382
```

Search completed: April 16, 2006, 01:39:37
Job time : 819 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 17:47:14 ; Search time 3806 Seconds
(without alignments)
221.274 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggaccctagagcgaag 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 300 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	656	2	BB629501 BB629501
2	18	100.0	674	5	BY727643 BY727643
3	18	100.0	668	2	BB613725 BB613725
4	18	100.0	2751	4	AK036566 Mus muscu
5	16.4	91.1	317	7	CK370327 zmtwv005
6	16.4	91.1	370	6	CF633642 zmtwv005
7	16.4	91.1	510	2	BE717998 PM1-HT079
8	16.4	91.1	704	10	AG354283 Mus muscu
9	16.4	91.1	744	8	DT058958 AGENCOURT
10	16.4	91.1	817	8	CX910994 UGI-CANAN
11	16.4	91.1	875	8	DT058819 AGENCOURT
12	16	88.9	296	2	BB247762 BB247762
13	16	88.9	396	2	BE768604 OYE-FT001
14	16	88.9	430	1	AT762325 wq97a04.x
15	16	88.9	507	3	BM029828 A88200.MA
16	16	88.9	538	10	AT208178 qg55a08.x
17	16	88.9	769	10	AG498153 Mus muscu
18	15.4	85.6	123	2	BE503972 h254a03.x
19	15.4	85.6	143	1	AI349272 ta55c07.x
20	15.4	85.6	170	1	AA654607 te59e02.8
21	15.4	85.6	177	1	AA234751 z838c05.8
22	15.4	85.6	205	1	AI099443 ue30f06.x

23	15.4	85.6	215	3	BI493189
24	15.4	85.6	241	9	BH084942
25	15.4	85.6	258	3	BI493190
26	15.4	85.6	288	2	BG384534 303762.MA
27	15.4	85.6	295	1	AA746945
28	15.4	85.6	296	1	AA747067 nx65d11.s
29	15.4	85.6	313	1	AM087244
30	15.4	85.6	326	3	BM743266
31	15.4	85.6	336	9	AZ801445
32	15.4	85.6	338	8	DN150252
33	15.4	85.6	348	5	BUG680671
34	15.4	85.6	350	1	AI678934
35	15.4	85.6	351	9	AZ430853
36	15.4	85.6	353	10	AG589928
37	15.4	85.6	364	7	CV310713
38	15.4	85.6	376	1	AA598484
39	15.4	85.6	377	5	BQ497250
40	15.4	85.6	387	1	AM013825
41	15.4	85.6	389	8	W60314
42	15.4	85.6	392	1	AI719432
43	15.4	85.6	392	3	BM504405
44	15.4	85.6	392	3	BM746356
45	15.4	85.6	393	1	AM301584
46	15.4	85.6	393	3	BM929646
47	15.4	85.6	397	1	AM392370
48	15.4	85.6	397	3	BM683597
49	15.4	85.6	399	2	BF109890
50	15.4	85.6	402	1	AI948978
51	15.4	85.6	402	2	BI120589
52	15.4	85.6	410	2	AA977744
53	15.4	85.6	413	2	BE570735
54	15.4	85.6	413	3	BM504184
55	15.4	85.6	416	1	AV759284
56	15.4	85.6	428	2	BF445861
57	15.4	85.6	429	1	AM891826
58	15.4	85.6	429	2	BF195828
59	15.4	85.6	431	2	BM710503
60	15.4	85.6	436	3	BM873461
61	15.4	85.6	442	7	CN310816
62	15.4	85.6	448	1	AI698018
63	15.4	85.6	449	1	AL537377
64	15.4	85.6	451	1	AA235149
65	15.4	85.6	458	1	AA781074
66	15.4	85.6	460	1	AA004225
67	15.4	85.6	472	2	BG700645
68	15.4	85.6	475	1	AL537378
69	15.4	85.6	476	6	CA866752
70	15.4	85.6	479	4	CR614418
71	15.4	85.6	488	3	BM930208
72	15.4	85.6	489	3	BM683685
73	15.4	85.6	490	6	CD237050
74	15.4	85.6	491	1	AV756616
75	15.4	85.6	497	10	CG850061
76	15.4	85.6	497	9	CC549348
77	15.4	85.6	498	3	BQ278252
78	15.4	85.6	499	3	BM507041
79	15.4	85.6	504	6	CB961454
80	15.4	85.6	504	6	CB991682
81	15.4	85.6	504	6	CB996192
82	15.4	85.6	504	6	CD110174
83	15.4	85.6	517	2	BG528700
84	15.4	85.6	517	3	BM746988
85	15.4	85.6	518	9	AQ412745
86	15.4	85.6	523	9	AO387177
87	15.4	85.6	525	3	BM845464
88	15.4	85.6	526	9	AZ065485
89	15.4	85.6	529	8	CX593974
90	15.4	85.6	542	3	BM822753
91	15.4	85.6	543	2	BF732540
92	15.4	85.6	547	3	BI787490
93	15.4	85.6	553	5	BU137811
94	15.4	85.6	559	3	BM822827
95	15.4	85.6	561	9	AZ392033

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BH084942	RPCI-24-2
BI493190	df98e07.y
BG384534	303762.MA
AA746945	nx65d11.s
AA747067	nx65d11.s
AM087244	xb97c11.x
BM743266	K-EST0016
AZ801445	2M0059122
DN150252	5238.H01
BUG680671	UI-CF-DU1
AI678934	tc99c04.x
AZ430853	1M0215E04
AG589928	Mus muscu
CV310713	CM0-FT004
AA598484	ae38f04.s
BQ497250	EST06479
AM013825	UI-H-B10-
W60314	zdzef02.b1
AI719432	ae64e10.x
BM504405	lh22e03.y
BM746356	K-EST0020
AM301584	xt98b04.x
BM929646	UI-E-E-J1-
AM392370	MR4-ST024
BM683597	UI-E-E-J1-
BF109890	7170h03.x
AI948978	wq17906.x
BI120589	F018P82.y
AA977744	OG48812.s
BE570735	7640e05.x
BM504184	ih22e03.x
AV759284	AV759284
BF445861	7b38c12.x
AM891826	CM3-NT008
BF195828	7b38c08.x
BM710503	7b38c05.x
BM873461	1aa12a09.
CN310816	170006001
AI698018	we19h08.x
AL537377	AL537377
AA235149	z838c05.x
AA781074	aj23808.s
AA004225	zh97d06.s
BG700645	602682256
AL537378	AL537378
CA866752	1r72a07.x
CR614418	full-1eng
BM930208	UI-E-E-J1-
BM683685	UI-E-E-J1-
CD237050	FNPACB03
AV756616	AV756616
CG850061	ZMBMB033
CC549348	CH240.433
BQ278252	AGENCOURT
BM507041	1h24a11.y
CB961454	AGENCOURT
CB991682	AGENCOURT
CB996192	AGENCOURT
CD110174	AGENCOURT
BG528700	602579593
BM746988	K-EST0021
AQ412745	RPCI-11-1
AO387177	RPCI-11-3
BM845464	K-EST0123
AZ065485	RPCI-23-4
CX593974	CT020007A
BM822753	K-EST0092
BF732540	nae12a11.
BI787490	sa146c11.
BU137811	603124903
BM822827	K-EST0093
AZ392033	1M0154P21

C 96	15.4	85.6	572	10	CE785184	C 169	15	83.3	175	1	AA151954
C 97	15.4	85.6	573	9	BZ539545	C 170	15	83.3	179	1	AA559544
C 98	15.4	85.6	574	7	CK905522	C 171	15	83.3	180	2	BI005692
C 99	15.4	85.6	577	9	AZ591114	C 172	15	83.3	182	1	AA481544
C 100	15.4	85.6	579	9	BZ539539	C 173	15	83.3	185	5	BU670987
C 101	15.4	85.6	579	11	CR16258	C 174	15	83.3	193	1	AA853831
C 102	15.4	85.6	580	5	BW148814	C 175	15	83.3	194	2	EG035839
C 103	15.4	85.6	596	9	AQ918955	C 176	15	83.3	201	1	AI720956
C 104	15.4	85.6	606	3	BM013427	C 177	15	83.3	206	1	AA353163
C 105	15.4	85.6	611	5	BO777182	C 178	15	83.3	209	9	BH311723
C 106	15.4	85.6	612	7	CK905521	C 179	15	83.3	213	1	AI434926
C 107	15.4	85.6	621	2	BB56765	C 180	15	83.3	215	1	AM103581
C 108	15.4	85.6	621	6	CD705000	C 181	15	83.3	217	7	CN260725
C 109	15.4	85.6	625	3	BM837637	C 182	15	83.3	225	1	AI182529
C 110	15.4	85.6	636	5	BK477723	C 183	15	83.3	226	1	AA459415
C 111	15.4	85.6	640	8	CX182808	C 184	15	83.3	226	8	H25788
C 112	15.4	85.6	642	7	CK005791	C 185	15	83.3	228	2	BE018221
C 113	15.4	85.6	649	9	CK757899	C 186	15	83.3	230	1	AI654782
C 114	15.4	85.6	653	10	CE755366	C 187	15	83.3	233	1	AI866432
C 115	15.4	85.6	664	9	BZ144650	C 188	15	83.3	239	2	BI021689
C 116	15.4	85.6	669	2	BF965563	C 189	15	83.3	243	1	AA506757
C 117	15.4	85.6	674	5	BM957150	C 190	15	83.3	250	1	AA758370
C 118	15.4	85.6	685	8	AG157422	C 191	15	83.3	250	1	AA494208
C 119	15.4	85.6	686	8	DN151938	C 192	15	83.3	251	1	AA552063
C 120	15.4	85.6	696	3	BI861828	C 193	15	83.3	251	1	AA370233
C 121	15.4	85.6	716	2	BF673545	C 194	15	83.3	253	1	AA961889
C 122	15.4	85.6	725	10	AG438387	C 195	15	83.3	255	6	CF130444
C 123	15.4	85.6	749	2	BF678820	C 196	15	83.3	257	1	AM874594
C 124	15.4	85.6	788	5	BUS32673	C 197	15	83.3	257	8	H25782
C 125	15.4	85.6	789	9	BH589808	C 198	15	83.3	264	3	BZ393561
C 126	15.4	85.6	792	11	CR108338	C 199	15	83.3	265	1	AI419779
C 127	15.4	85.6	809	9	CC358190	C 200	15	83.3	271	1	AA952963
C 128	15.4	85.6	813	5	BUS37587	C 201	15	83.3	274	2	BI021698
C 129	15.4	85.6	813	9	BH107451	C 202	15	83.3	275	1	AA878251
C 130	15.4	85.6	835	6	CA477221	C 203	15	83.3	275	1	AA532661
C 131	15.4	85.6	843	5	CC720645	C 204	15	83.3	282	1	AA514511
C 132	15.4	85.6	845	5	BQ424436	C 205	15	83.3	284	1	AM015934
C 133	15.4	85.6	848	5	BQ431499	C 206	15	83.3	284	2	BI089025
C 134	15.4	85.6	857	11	CR079620	C 207	15	83.3	286	1	AM338581
C 135	15.4	85.6	858	9	BZ539723	C 208	15	83.3	292	1	AI673126
C 136	15.4	85.6	871	2	BF675225	C 209	15	83.3	293	1	AM068093
C 137	15.4	85.6	872	6	CD515594	C 210	15	83.3	305	1	AA502726
C 138	15.4	85.6	876	5	BU189739	C 211	15	83.3	311	3	BP385395
C 139	15.4	85.6	881	5	BX361165	C 212	15	83.3	314	3	BM768553
C 140	15.4	85.6	885	5	BO232385	C 213	15	83.3	315	1	AM516667
C 141	15.4	85.6	886	5	BK416924	C 214	15	83.3	318	1	AI278707
C 142	15.4	85.6	911	5	BX328031	C 215	15	83.3	318	1	AA508653
C 143	15.4	85.6	924	2	BE540523	C 216	15	83.3	318	2	BI021700
C 144	15.4	85.6	931	10	CM924982	C 217	15	83.3	322	1	AI248883
C 145	15.4	85.6	931	10	CG067841	C 218	15	83.3	322	5	EX473513
C 146	15.4	85.6	936	2	BF165108	C 219	15	83.3	330	1	AM591773
C 147	15.4	85.6	945	2	BG110396	C 220	15	83.3	334	1	AA506454
C 148	15.4	85.6	951	5	BO880107	C 221	15	83.3	337	7	T40539
C 149	15.4	85.6	973	10	CG921167	C 222	15	83.3	338	1	AM182773
C 150	15.4	85.6	1000	10	CG365229	C 223	15	83.3	338	1	AA479918
C 151	15.4	85.6	1015	5	BU327923	C 224	15	83.3	339	1	AI965104
C 152	15.4	85.6	1024	5	BG029496	C 225	15	83.3	339	2	BE908524
C 153	15.4	85.6	1046	6	CB961870	C 226	15	83.3	340	1	AI077915
C 154	15.4	85.6	1096	1	AL515292	C 227	15	83.3	342	2	BF939440
C 155	15.4	85.6	1120	1	AL535154	C 228	15	83.3	348	1	BF939440
C 156	15.4	85.6	1167	9	CC268116	C 229	15	83.3	348	1	AI502186
C 157	15.4	85.6	1303	8	DN685116	C 230	15	83.3	348	1	AI502186
C 158	15.4	85.6	1420	10	CL646896	C 231	15	83.3	350	1	AA835477
C 159	15.4	85.6	1450	4	AK051544	C 232	15	83.3	355	1	AA641534
C 160	15	83.3	125	1	AA938023	C 233	15	83.3	360	6	CA153872
C 161	15	83.3	128	1	AA285031	C 234	15	83.3	362	2	BG994684
C 162	15	83.3	134	8	W42749	C 235	15	83.3	363	1	AA953293
C 163	15	83.3	150	1	AI128633	C 236	15	83.3	363	1	AA484009
C 164	15	83.3	156	6	CD177653	C 237	15	83.3	364	1	AA473294
C 165	15	83.3	159	1	AA860424	C 238	15	83.3	367	1	AM665209
C 166	15	83.3	159	1	AA327953	C 239	15	83.3	370	2	BG752518
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C 168	15	83.3	172	7	CN260722	C 241	15	83.3	371	8	W42436

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AA853831	NHTBGAe09
BG035839	602325931
AI720956	ab79109.x
AA353163	EST61302
BH311723	CH230-26H
AI434926	LI38B08.x
AM103581	xe78b09.x
CN260725	170005999
AI828290	wa84h09.x
AA459415	zx89h05.b
H25788	y149b05.x1
BE018221	db77b07.y
AI654782	wb49902.x
AI866432	wk18c09.x
BI021689	CN3-MT034
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AA758370	z945901.b
AA494208	n999f08.b
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AA370233	EST81819
AA961889	or44d11.b
CF130444	UI-HF-BSO
AM874594	h066a12.x
H25782	y149a06.x1
BZ393561	BP393561
AI419779	tg99e12.x
AA952963	CN3-C09.8
BI021698	CN3-MT034
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AA532661	nj45a03.s
AA514511	nf62c05.s
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BI089025	602853575
AM338581	xw72a10.x
AI673126	we71c01.x
AM068093	cn23b03.x
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BM768553	K-EST0051
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AA506454	n11h10.b
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AM182773	xp97e08.x
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AI965104	wx35907.x
BE908524	601501384
AI077915	oy15c11.s
BF939440	nad89909.f
AI086019	oy70f05.x
AI523186	at65908.x
AA303091	EST12940
AA835477	ak79a04.s
CA153872	SCVPR2203
BG994684	PM2-HT128
AA953293	oc74a04.s
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AA473294	xy23h07.x
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BG752518	602731021
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C 252	15	83.3	393.3	CR612702	CR612702 full1-1eng
C 253	15	83.3	393.5	BX421021	BX421021 BX421021
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C 255	15	83.3	394.1	AI1222030	AI1222030 qh01g04.x
C 256	15	83.3	397.1	AA699459	AA699459 z143C10.s
C 257	15	83.3	397.8	TS7831	TS7831 ycl4f12.s1
C 258	15	83.3	398.1	AA961603	AA961603 op30g08.s
C 259	15	83.3	399.1	AI076417	AI076417 oz09d08.x
C 260	15	83.3	400.1	AI018617	AI018617 oc91d08.s
C 261	15	83.3	402.1	AA464265	AA464265 xs81d10.s
C 262	15	83.3	403.1	AI091825	AI091825 xs58c05.s
C 263	15	83.3	403.9	AQ118529	AQ118529 HS_3011.B
C 264	15	83.3	405.1	AA806590	AA806590 ob67g03.s
C 265	15	83.3	405.1	AA523728	AA523728 ng31b03.s
C 266	15	83.3	405.5	BU730512	BU730512 UI-E-C11-
C 267	15	83.3	413.1	AI1299967	AI1299967 qo24b02.x
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C 269	15	83.3	414.1	AA837993	AA837993 ce68b11.s
C 270	15	83.3	415.1	AI080097	AI080097 cz36a07.x
C 271	15	83.3	417.6	CF382840	CF382840 q236h01.
C 272	15	83.3	418.1	AI124834	AI124834 qh70e04.x
C 273	15	83.3	420.1	AI1354517	AI1354517 yu46g02.x
C 274	15	83.3	420.8	N33480	N33480 yy42d10.s1
C 275	15	83.3	421.1	AA065082	AA065082 zml3a04.s
C 276	15	83.3	426.1	AI1744302	AI1744302 t09pa10.x
C 277	15	83.3	427.7	CNI137433	CNI137433 OX1_57.F0
C 278	15	83.3	428.1	AI606877	AI606877 tw84e06.x
C 279	15	83.3	429.1	AA999919	AA999919 oc02b11.s
C 280	15	83.3	432.8	W86074	W86074 zd91c09.s1
C 281	15	83.3	433.1	AA723811	AA723811 ah87f02.s
C 282	15	83.3	433.3	AA548418	AA548418 nj14g08.s
C 283	15	83.3	433.3	BM709842	BM709842 UI-E-C01-
C 284	15	83.3	435.1	AI1445510	AI1445510 t130a09.x
C 285	15	83.3	436.2	BG223171	BG223171 nahe5c02.
C 286	15	83.3	437.1	AA458972	AA458972 zx88g07.s
C 287	15	83.3	440.8	RS4623	RS4623 yj174905.s1
C 288	15	83.3	442.5	BU935555	BU935555 AGENCOURT
C 289	15	83.3	445.10	CE428666	CE428666 t1igr-gss
C 290	15	83.3	445.1	AI1446090	AI1446090 t131f09.x
C 291	15	83.3	447.1	AI0322723	AI0322723 ox11f04.x
C 292	15	83.3	448.1	AI1300503	AI1300503 qo11c10.x
C 293	15	83.3	454.1	AA291557	AA291557 zt45e04.s
C 294	15	83.3	457.1	AA533309	AA533309 nj65g04.s
C 295	15	83.3	459.1	AI168496	AI168496 ou64h05.s
C 296	15	83.3	461.1	AI1761144	AI1761144 wh97h01.s1
C 297	15	83.3	461.8	N26709	N26709 yv61c12.x
C 298	15	83.3	462.5	BU734139	BU734139 UI-E-CQ1-
C 299	15	83.3	466.1	AI124347	AI124347 qx92e11.x
C 300	15	83.3	467.5	BU508676	BU508676 AGENCOURT

RESULT 1	BB629501	656 bp	mRNA	linear	EST 31-AUG-2001
LOCUS	BB629501				
DEFINITION	BB629501	RIKEN full-length enriched, adult male bone	Mus musculus		
	cDNA clone 9830134F20 5', mRNA sequence.				
ACCESSION	BB629501				
VERSION	BB629501.1	GI:15399640			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				

ALIGNMENTS

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 656)

REFERENCE
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiemoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J.,
Kono,H., Konda,M., Koya,S., Matsumura,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiaki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)

TITLE
JOURNAL

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Shohiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalisation and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,K., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
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Funct. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
SOURCE
Location/Qualifiers
1. 656
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_id="9830134F20"
/sex="male"
/tissue_type="bone"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male bone"
/note="Site 1: Salt. Site 2: BamHI, cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 5'
GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3', cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence 5' GAGAGAGAGATTCGAGCTTAATTAAATTAAATACCCCCCCCCCCCC
3'. cDNA was cleaved with XhoI and BamHI. Vector: a

modified Bluescript KS(+) after bulk excision from Lambda
FLC I."

Query Match 100.0%; Score 18; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGACCTAGAGCAAG 18
|||||
345 CGGACCTAGAGCAAG 362

RESULT 2
LOCUS B727643
DEFINITION B727643 RIKEN full-length enriched, 6 days neonate medulla oblongata Mus musculus cDNA clone B730020D01 5', mRNA sequence.

ACCESSION B727643
VERSION B727643
KEYWORDS GI:27140770

SOURCE Mus musculus (house mouse)

REFERENCE
AUTHORS

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 674)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Ose, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schomach, C., Gotohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Baralov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kaul, J., Kaul, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawachi, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sander, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszewski, B. A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kizawa, T., Kono, H., Koyama, S., Koyama, S., Miyazaki, A., Murata, N., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohno, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, M., Muramatsu, M., and Hayashizaki, Y.

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Carninci, P., Imocani, K., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kizawa, T., Kono, H., Koyama, S., Miyazaki, A., Murata, N., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohno, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, M., Muramatsu, M., and Hayashizaki, Y.

FEATURES
source

Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

1. 674
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="B730020D01"
/tissue_type="medulla oblongata"
/dev_stage="6 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 6 days neonate medulla oblongata"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
GAGAGGAGAGATTCAGAGCTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trihaloethane thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGGAGATTCAGAGCTCTTTTCTTTTCTTTT 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 674;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGACCTAGAGCAAG 18
|||||
241 CGGACCTAGAGCAAG 258

RESULT 3
LOCUS BB613725
DEFINITION BB613725 RIKEN full-length enriched, 0 day neonate head Mus musculus cDNA clone 483141M17 5', mRNA sequence.

ACCESSION BB613725
VERSION BB613725.1 GI:15395652
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 688)
Aizawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,

COMMENT

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp), URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>,
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

Source

1. 2751
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM:DB:9830134F20"
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/clone="9830134F20"
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/tissue_type="bone"
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/dev_stage="adult"
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/note="kinase suppressor of ras (MGD) MGI:105051, GBNM_013571, evidence: BLASTN, 100%, match=1985"

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 2751;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGACCTTAGGCGAAG 18
|||||

345 CGGACCTTAGGCGAAG 362

RESULT 5

CK370327/c CK370327 317 bp mRNA linear EST 23-DEC-2003
DEFINITION zmrw005.0A10-002-b11.s0 zmrw005 Zea mays cDNA 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

AUTHORS

1 (bases 1 to 317)
Bohner, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredrickson, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y., and Nguyen, H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Signaling under Drought

JOURNAL

COMMENT

Unpublished (2003)
Contact: Hans Bohner
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohner@life.uiuc.edu
POLYA=No.

FEATURES

Source

Location/Qualifiers
1. 317
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="zmrw005"
/note="Library zmrw005 consists of the same cDNA

material as library zmrw00 (described below) but was sequenced from the 5' prime end. The sequence identifier uses the 's0' suffix because the library tag was at the 3' prime end and thus not identified. Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) and low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw05 and zmrw48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohner (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, DS: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)⁺mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)⁺mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adsorbed with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E. coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 10⁶; zmrw48: 4.87 x 10⁶; zmrw00: 3 x 10⁶. The background of empty clones was less than 1%. Inserts ranged from -0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30°C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw05: 2.0x10⁷; zmrw48: 4.2x10⁷; zmrw00: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R.E.; Silk W.K.; Hsiao T.C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W.G.; Lenoble M.E.; Samuels T.D.; Bernsein N.; Sharp R.E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March,

ORIGIN

2000. 967-976.
TAG_TISSUE=Not found
TAG_SEQ=Not found"

Query Match 91.1%; Score 16.4; DB 7; Length 317;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
D0 41 CGGACCTAGAGGCAAG 24

RESULT 6
LOCUS CF633642
DEFINITION CF633642 370 bp mRNA linear EST 02-OCT-2003
ACCESSION CF633642
VERSION CF633642.1 GI:37392777
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

Bohner, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredrickson, M.,
Bohner, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A.,
Topinka, C., Davis, G.E., Schachtman, D., Wu, Y., and Nguyen, H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
Signaling Under Drought
Unpublished (2003)

JOURNAL

University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohner@life.uiuc.edu
POLYA=No.

COMMENT

FEATURES

source

location/Qualifiers
1..370

/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"

/clone_lib="zmrw000"

/note="Samples were collected in Robert E. Sharp's lab
(University of Missouri-Columbia) to construct three
normalized cDNA libraries. Dark-grown maize seedlings with
primary roots 12-20 mm in length were transplanted to high
(-0.03 MPa) or low water potential (-1.6 MPa) vermiculite,
and harvested at 5 h and 48 h after transplanting. About
1,000 roots were used for each of the low water potential
libraries (zmrw005 and zmrw048) while 500 roots were
combined from each of the two time points at high water
potential (zmrw000). Each root was divided into 4 segments
(distances are from the junction of the root apex and root
cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7
mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details
of conditions see (1)) with nutrient modifications as in
(2). The three normalized cDNA libraries were constructed
in the lab of Hans Bohner (University of Illinois-UC).
Total RNA was extracted by the 'hot phenol' method (Plant
Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This
method worked in eliminating carbohydrate material present
in the root tips. The integrity of the RNA was verified by
denaturing agarose gels and spectrophotometry (ratio
A260/A280). Poly(A)+mRNA was isolated twice from total RNA
using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+ mRNA
was converted to double-stranded cDNA and tagged by using
modified oligo(dT) primers. One of 4 sequence tags
corresponding to a different segment of the root was added
to the 3'-end of the modified oligo(dT) primers, including

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 370;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAG 18
D0 255 CGGACCTAGAGGCAAG 272

RESULT 7

LOCUS BE717998 510 bp mRNA linear EST 12-SEP-2000
DEFINITION PM1-HT0790-250600-001-809 HT0790 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE717998
VERSION BE717998.1 GI:10106263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

Dias Neto, E., Garcia Correa, R., Veizovskii-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

a NotI site and used to reverse transcribe the
segment-specific mRNAs into cDNAs. Each library contains
all four tags. A suffix (s1, s2, s3 or s4) has been added
to each sequence identifier to designate which region of
the root (Root segment 1, 2, 3, or 4) the sequence was
found in based on the identification of the tag. A suffix
of s0 indicates that the sequence tag, and hence the
source segment, could not be identified. The double
stranded cDNAs were size-selected (>450 bp). Size selected
cDNAs were adapted with EcoRI adaptors at both ends, and
then digested with NotI. The cDNA was directionally cloned
into EcoRI-NotI digested pBS II SK(+) phagemid vector
(Stratagene) and electroporated into E.coli DH10b. The
total number of white colony forming units (cfu) in the
primary libraries before amplification was as follows:
zmrw005: 3.37 x 10⁶; zmrw048: 4.87 x 10⁶; zmrw00: 3 x
10⁶. The background of empty clones was less than 1%.
Inserts ranged from ~0.5 kb to ~2.5 kb, as determined by
PCR. Plasmid DNA from the primary libraries then was
converted to single-stranded circles and used as a
template for PCR amplification using the T7 and T3 priming
sites that flank the cloned cDNA inserts. The purified PCR
products, representing the entire cDNA population cloned
in each library, were used as a driver for normalization.
Hybridization between the single-stranded library and the
PCR products was carried out for 44 hours at 30°C.
Non-hybridized single-stranded DNA circles were separated
from hybridized DNA rendered partially double-stranded and
electroporated into DH10b. The total number of clones with
insert was: zmrw005: 2.0x10⁷; zmrw048: 4.2x10⁷; zmrw00:
1.1x10⁷. The background of empty clones was less than 2%.
Insert size, determined by PCR of the entire library,
ranged from 0.5 kb to 2.5 kb. (1) Sharp R.E., Silk W.K., Hsiao
T.C. Growth of the Maize Primary Root at Low Water
Potentials I. Spatial Distribution of Expansive Growth.
Plant Physiology (Rockville). 87(1). 1988. 50-57. (2)
Spollen W.G., Lenoble M.E., Samuels T.D., Bernstein N., Sharp
R.E. Abscisic acid accumulation maintains maize primary
root elongation at low water potentials by restricting
ethylene production. Plant Physiology (Rockville). 122(3).
March, 2000. 967-976.
TAG_TISSUE=Not found
TAG_SEQ=Not found"

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PIBMBD 1073780

COMMENT Contact: Simpson A.U.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES

source 1..510
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0790"
/note="Organ: head neck; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Location/Qualifiers
High quality sequence start: 429.
High quality sequence stop: 429.
Seq primer: puc 18 forward
Location/Qualifiers

ORIGIN

Query Match 91.1%; Score 16.4; DB 2; Length 510;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTTAGAGCAAG 18
|||||
443 CAGACCTTAGAGCAAG 426

RESULT 8
AG354283 704 bp DNA linear GSS 18-DEC-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-152G07.T7, genomic survey sequence.
ACCESSION AG354283
VERSION AG354283.1 GI:47927593
KEYWORDS GSS
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K., and Shitohshi, T.
Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
JOURNAL 1574823
PUBMED 2 (bases 1 to 704)
REFERENCE Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
TITLE Submitted (17-NOV-2003) Masahito Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/)

COMMENT Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R Site 1 : EcoRI
R Site 2 : EcoRI
Location/Qualifiers
1..704
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-152G07.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 704;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTTAGAGCAAG 18
|||||
426 CGGACCTTAGAGCAAG 443

RESULT 9
DT058958 744 bp mRNA linear EST 11-AUG-2005
LOCUS AGENCOURT 55789292 NICHG XGC_Fab Xenopus laevis cDNA clone
DEFINITION IMAGE:8069448 5', mRNA sequence.
DT058958
ACCESSION DT058958.1 GI:72358207
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 744)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: CGAPbs-rc@mail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM17342 row: d column: 22
High quality sequence stop: 623.
Location/Qualifiers

FEATURES

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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8069448"
/lab_host="DH10B Tora"

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Conventions EST name is generated by the concatenation of
Clone id and the direction of sequencing. The suffix ".fwd"
is a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
library sequence stop: 752.
Location/Qualifiers
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/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="RMAGE:7688136"
/sex="male"
/tissue_type="Testes"
/dey_stage="Adult"
/lab_host="ElectromAX DH10B"
/clone_lib="NH XGC_cryptea"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
this library was made from dt primed cDNA and cloned into

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Query Match	91.1%;	Score 16.4;	DB 8;	Length 875;
Similarity	94.4%;	Pred. No. 1.3e+03;		
Best Local	0;	Mismatches 1;	Indels 0;	Gaps 0;
Matches 17;	Conservative			

Qy 1 CGACCTAGAGGCAAG 18
 |||||
 Db 498 CGACCTAGAGGCAAG 481

RESULT 12
 BB247762 296 bp mRNA linear EST 06-JUL-2000
 LOCUS BB247762 RIKEN full-length enriched, 7 days neonate cerebellum Mus
 DEFINITION musculus cDNA A730021A22 3', mRNA sequence.
 BB247762
 ACCESSION BB247762 GI:8940508
 VERSION BB247762.1 GI:8940508
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
 Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Oda, H.,
 Okazaki, Y., Ono, T., Owa, C., Saito, H., Mizuno, Y., Nakamura, M., Oda, H.,
 Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T.,
 Soabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
 Terahashi, F., Tomioka, N., Toyota, T., Tsunoda, Y., Watanabe, S.,
 Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
 Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
 Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al.)
 Unpublished (2000)

TITLE
 JOURNAL Contact: Yoshihide Hayashizaki
 COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,
 Saeki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 The isolation and characterization of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kikuchi, T., Akiyama, J., Shibata, K., Iizawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 SOURCE Location/Qualifiers
 1..296
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A730021A22"
 /tissue_type="cerebellum"
 /dev_stage="7 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 7 days neonate
 cerebellum"
 /note="Site 1: SalI; Site 2: BamHI. cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken

Query Match 88.9%; Score 16; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGACCTAGAGGCAAA 17
 |||||
 Db 50 CGACCTAGAGGCAAA 65

RESULT 13
 BE768604/c 396 bp mRNA linear EST 20-SEP-2000
 LOCUS BE768604 QV2-F70010-090800-303-b06 F70010 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE768604
 ACCESSION BE768604.1 GI:10222262
 VERSION BE768604.1 GI:10222262
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

TITLE
 JOURNAL 1 (bases 1 to 396)
 COMMENT Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-27049222
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPER/P/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?litr-at2-QV2-F70010-090
 800-303-b06&t3=2000-08-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 384.

FEATURES
 SOURCE Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="F70010"
 /note="Organ: prostate tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORFESTS PCR (U.S. Letters Patent Application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under

contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATCTCGAGTTATTTATTTATCCCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from lambda
 FLC I."

ORIGIN low stringency conditions."

Query Match 88.9%; Score 16; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACCTAGAGGCAAA 16
|||||
49 CGGACCTAGAGGCAAA 34

RESULT 14
A1762325/c 430 bp mRNA linear EST 20-DEC-1999
LOCUS
DEFINITION wg97a04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2379150 3',
mRNA sequence.
A1762325
VERSION A1762325.1 GI:5177992
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 430)
NCI CGAP htcp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-rt@mail.nih.gov
Tissue Procurement: Christopher Moskalik, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bdrip/image/image.html
Insert Length: 574 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
1. 430
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2379150"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and 98 circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clones 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Facina Bonaldo."

ORIGIN

Query Match 88.9%; Score 16; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAA 17
|||||
36 GGACCTAGAGGCAAA 21

RESULT 15

EM029828 507 bp mRNA linear EST 05-NOV-2001
LOCUS
DEFINITION 488200 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION EM029828
VERSION EM029828.1 GI:16743398
KEYWORDS
SOURCE EST.
ORGANISM Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Smith, T.P.L., Grose, M.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Cassas, E., Wray, J.E., White, J., Cho, J., Fahrnenking, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-Mckown, C.G., Petrea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keesle, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 118 row: A column: 17
Seq primer: ATTAGGTGACTACTAG.
Location/Qualifiers
1. 507
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from testis, thymus,
semiteendous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

FEATURES

source

Query Match 88.9%; Score 16; DB 3; Length 507;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
|||||
29 GGACCTAGAGGCAAG 45

RESULT 16
A1208178/c 538 bp mRNA linear EST 30-NOV-1998
LOCUS
DEFINITION g955a08.x1 Soares, teatis NHT Homo sapiens cDNA clone IMAGE:1839062
3' similar to gb:158603 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT
(HUMAN); mRNA sequence.
A1208178
VERSION A1208178.1 GI:3770120
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 538)

ORIGIN

Query Match 88.9%; Score 16; DB 3; Length 507;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
 Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution by: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbtp/image/image.html
 Insert Length: 639 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 431.
 Location/Qualifiers

FEATURES
source

```
1..538
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:1839062"
  /sex="male"
  /lab_host="DH10B"
  /clone_lib="Soares testis_NHT"
  /note="vector: pT7T3D-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5',
TGTTCACATCTGAAGTGGAGCGCCGCCCAATTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Query Match 88.9%; Score 16; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACCTAGAGGCAAA 17
 |||||
Db 528 GGACCTAGAGGCAAA 513

RESULT 17

AG498153 769 bp DNA linear GSS 22-DEC-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-397021.T7, genomic survey
DEFINITION sequence.

ACCESSION AG498153
VERSION AG498153.1 GI:48205383
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
 Ezawa, K., Satou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and
 Shiohishi, T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823

REFERENCE 2 (bases 1 to 769)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Substitution
JOURNAL Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical

COMMENT

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
 (E-mail: hattori@sc.riken.jp, URL: <http://hgp.gsc.riken.go.jp/>,
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center.
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp

FEATURES**source**

```
1..769
  /organism="Mus musculus molossinus"
  /mol_type="genomic DNA"
  /sub_species="molossinus"
  /db_xref="taxon:57486"
  /clone="MSMg01-397021.T7"
  /sex="male"
  /tissue="mixture of kidney and spleen"
  /clone_lib="MSMg01 Mouse Male BAC Library"
```

ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 769;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACCTAGAGGCAAG 18
 |||||
Db 160 GACCTAGAGGCAAG 175

RESULT 18

BE503972 123 bp mRNA linear EST 04-AUG-2000
LOCUS h254a03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:1211756 3',
DEFINITION mRNA sequence.

ACCESSION BE503972
VERSION BE503972.1 GI:9706380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
 Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution by: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 104.
 Location/Qualifiers

FEATURES**source**

```
1..123
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
```

/clone="IMAGE:3211756"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu24"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lus was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 85.6%; Score 15.4; DB 2; Length 123;
 Best Local Similarity 94.1%; Pred. No. 3.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTTAGAGGCAAG 18
 |||||||||
 51 GGACCTTAGAGGCCAAG 67

RESULT 19
 A1349272/c 143 bp mRNA linear EST 16-FEB-1999
 LOCUS ta75c07.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2049900 3',
 mRNA sequence.
 A1349272
 A1349272.1 GI:4086478
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 143)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 236 Std Error: 0.00
 Seq primer: -40UP from Gibco.

FEATURES

Source
 1. 143
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2049900"
 /tissue_type="stem cell 34+/38+"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP HSC2"
 /note="Organ: bone marrow; Vector: pAMP1; mRNA made from bone marrow, stem cells 34+/38+, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 143;
 Best Local Similarity 94.1%; Pred. No. 3.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GGACCTTAGAGGCAAG 18
 |||||||||
 58 GGACCTTAGAGGCCAAG 42

RESULT 20
 AA654607 170 bp mRNA linear EST 04-NOV-1997
 LOCUS aa59e02.g1 NCI_CGAP_P33 Homo sapiens cDNA clone IMAGE:1202810, mRNA
 sequence.
 AA654607
 AA654607.1 GI:2590761
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

ORIGIN

REFERENCE 1 (bases 1 to 170)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui,
 M.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40m13 fwd. Et from Amersham
 High quality sequence stop: 142.

FEATURES

Source
 1. 170
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1202810"
 /sex="Male"
 /dev_stage="45 Years old"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP P33"
 /note="Vector: pAMP10; Site_1: NotI, Site_2: EcoRI; 1st strand cDNA was primed with oligo (dT) 17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDP-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 170;
 Best Local Similarity 94.1%; Pred. No. 3.8e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTTAGAGGCAAG 18
 |||||||||
 65 GGACCTTAGAGGCCAAG 81

RESULT 21
 AA234751 177 bp mRNA linear EST 03-MAR-1997
 LOCUS AA234751

DEFINITION z38c05.s1 Soares NHPu_S1 Homo sapiens cDNA clone IMAGE:687464
3', mRNA sequence.

ACCESSION AA234751
AA234751.1 GI:1859468

KEYWORDS EST.
Homo sapiens (human)

SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 177)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 157.
Location/Qualifiers

FEATURES
source 1..177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5591614"
/db_xref="taxon:9606"
/clone="IMAGE:687464"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NHPu_S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker. Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bHM, pregnant uterus
NHPu, and fetal heart NHPu19w) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260332-265223,
340488-345479, and 484488-489479."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 177;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGAGGCAAG 18
|||||
Db 53 GGACCTAGAGGCCAAG 69

RESULT 22
AI099443 205 bp mRNA linear EST 20-AUG-1998
LOCUS AI099443
DEFINITION uc30f06.x1 Sugano mouse liver mla mus musculus cDNA clone
IMAGE:148191.3' similar to SW:ALBU_Rat F02770 SERUM ALBUMIN
PRECURSOR. [1], mRNA sequence.

ACCESSION AI099443
AI099443.1 GI:3448968

VERSION EST.
MUS musculus (house mouse)

KEYWORDS Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 205)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:930247
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..205
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1481891"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mla"
/note="Organ: liver; Vector: pME18S-Fl3; Site 1: DraIII
(CACTGTCG); Site 2: DraIII (CACCATGCG); 1st strand cDNA
was primed with an oligo (dt) primer
[ATGTGACCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGCCTGTCG), digested
and cloned into distinct DraIII sites of the pME18S-Fl3
vector (5' site CACTGTCG, 3' site CACCATGCG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGCTCTTAAAGTCGCG and 3' end
primer CGACTGTCAGTCGACACA."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 205;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCTAGAGGCATA 17
|||||
Db 27 CGATCCTAGAGGCATA 11

RESULT 23
BI493189 215 bp mRNA linear EST 28-AUG-2001
LOCUS BI493189
DEFINITION d598e07.w1 Morton fetal cochlea Homo sapiens cDNA clone
IMAGE:2540629.3', mRNA sequence.

ACCESSION BI493189
BI493189.1 GI:15332533

VERSION EST.
Homo sapiens (human)

KEYWORDS Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 215)

AUTHORS

Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening

JOURNAL

Genomics 23, 42-50 (1994)

COMMENT

Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996

Email: cmorton@rics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLM6328 row: 1 column: 14
Seq primer: T7 primer.

FEATURES

source

Location/Qualifiers

1..215
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2540629"
/tissue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Morton Fetal Cochlea"
/note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dt. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' GAATTCGACGACG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 215;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18

Db 28 GGACCTTAGAGGCAAG 44

RESULT 24 241 bp DNA linear GSS 18-JUL-2001
BH084942/c
LOCUS
DEFINITION
RPCI-24-236H6.TV RPCI-24 Mus musculus genomic clone RPCI-24-236H6.
Genomic survey sequence.

ACCESSION
BH084942

VERSION
BH084942.1 GI:14904539

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 241)
Zhao, S., Nieman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shwartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)

Other GSSs: RPCI-24-236H6.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@ligr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdjong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.ligr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 236 row: H column: 6
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..241
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-236H6"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 241;
Best Local Similarity 94.1%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTTAGAGGCAAA 17

Db 203 CGGACCTTAGAGGTAAA 187

RESULT 25 258 bp mRNA linear EST 28-AUG-2001
BI493190/c
LOCUS
DEFINITION
dF98607.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2540629 5', mRNA sequence.

ACCESSION
BI493190

VERSION
BI493190.1 GI:15332534

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 258)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening

Genomics 23, 42-50 (1994)

7829101

Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996

Email: cmorton@rics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLM6328 row: I column: 14
Seq primer: M13R1 reverse primer (ABI).
Location/Qualifiers

SOURCE

1. .258
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540629"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcorI; Site 2: XhoI; Reference: Genomics 23, 42-50, (1994) Cloned unidirectionally. Primer: Oligo dt. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. ~5' adaptor sequence: 5' GAATTCGGCAGCG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 258;
 Best Local Similarity 94.1%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
 |||||
 DB 188 GGACCTAGAGCCAG 172

RESULT 26

BG384534 288 bp mRNA linear EST 12-MAR-2001
 LOCUS 303762 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION BG384534
 VERSION BG384534.1 GI:13309078
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

REFERENCE

1 (bases 1 to 288)
 Fahrnkung, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
 Vallet, J., Wise, T., Rohrer, G.A., Petrea, G., Sultana, R.,
 Quackenbush, J., and Keeler, D.W.
 Porcine gene discovery by normalized cDNA-library sequencing and
 EST cluster assembly
 Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL PUBLISHED
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smitht@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mismatches 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACGCTATGACCAT
 BACKWARD: GTTTCCTCATCGACGAG
 Plate: 92 row: B column: 1
 Seq primer: ATTAGGTGACCTATAG.

FEATURES

SOURCE

1. .288
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 1P1G"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryo."

ORIGIN

Query Match 85.6%; Score 15.4; DB 2; Length 288;
 Best Local Similarity 94.1%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
 |||||
 DB 77 GGACCTAGAGCCAG 61

RESULT 27

AA746945 295 bp mRNA linear EST 16-JAN-1998
 LOCUS 1662105.81 NCI_CGAP_Alvi Homo sapiens cDNA clone IMAGE:1266873,
 DEFINITION mRNA sequence.
 ACCESSION AA746945
 VERSION AA746945.1 GI:2786903
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

1 (bases 1 to 295)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.

JOURNAL

CDNA Library Preparation: David B. Kitzman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www.bio.lim.gov/bdrip/image/image.html
 Seq primer: -40ml3 fwd. RT from Amersham.

FEATURES

SOURCE

1. .295
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1266873"
 /tissue_type="alveolar rhabdomyosarcoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Alvi"
 /note="Vector: pAMP10; mRNA made from alveolar
 rhabdomyosarcoma, cDNA made by oligo-dT priming.
 Non-directionally cloned. Size-selected on agarose gel,
 average insert size 600 bp. Reference: Kitzman et al.
 (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 295;
 Best Local Similarity 94.1%; Pred. No. 4e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGCAAG 18
 |||||
 DB 62 GGACCTAGAGCCAG 78

RESULT 28

AA747067 296 bp mRNA linear EST 07-FEB-1998
 LOCUS 1665411.81 NCI_CGAP_Alvi Homo sapiens cDNA clone IMAGE:1267125,
 DEFINITION mRNA sequence.
 ACCESSION AA747067
 VERSION AA747067.1 GI:2787025
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORIGIN

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE 1 (bases 1 to 296)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Insert Length: 371 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

FEATURES
source
1..296
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1267125"
/tissue_type="alveolar rhabdomyosarcoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Alve1"
/note="Vector: pAMP10; mRNA made from alveolar
rhabdomyosarcoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Reference: Krizman et al.
(1996) Cancer Research 56:5380-5383."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 296;
Best Local Similarity 94.1%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
|||||
62 GGACCTTAGAGGCAAG 78

RESULT 29
LOCUS AM087244 313 bp mRNA linear EST 15-OCT-1999
DEFINITION X097c11.X1 NCI CGAP Co21 Homo sapiens cDNA clone IMAGE:2582708 3',
mRNA sequence.
ACCESSION AM087244
VERSION AM087244.1 GI:6043049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 313)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskajuk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bdrrp/image/image.html
Possible reversed clone: polyT not found
Seq primer: -40UP from Glibco
High quality sequence stop: 301.
Location/Qualifiers
1..313
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2582708"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co21"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; cloned undirectionally. Primer: Oligo dT.
Normalized to Cot >500. Average insert size 1.04kb.
Normalized version of NCI CGAP Co18. Library constructed
by Life Technologies."

ORIGIN
Query Match 85.6%; Score 15.4; DB 1; Length 313;
Best Local Similarity 94.1%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTTAGAGGCAAG 18
|||||
270 GGATCCTTAGAGGCAAG 254

RESULT 30
LOCUS BM743266 326 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0016364 S4SNUI Homo sapiens cDNA clone S4SNUI-10-E01 5', mRNA
sequence.
ACCESSION BM743266
VERSION BM743266.1 GI:19064595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 326)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, D.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 10 row: E column: 01
High quality sequence stop: 326.
Location/Qualifiers
1..326
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S4SNUI-10-E01"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab_host="Top10P"
/clone_lib="S4SNUI"
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; the poly (A) RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped

with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 326;
Best Local Similarity 94.1%; Pred. No. 4e+03; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Oy 2 GGACCTAGAGGCAAG 18
|||
Db 115 GGACCTAGAGGCCAAG 99

Search completed: April 15, 2006, 18:51:14
Job time : 3827 secs